

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 141074

TO: Andrew D Kosar

Location: REM/3C04/3C18

Art Unit: 1654

Search Notes

Monday, January 03, 2005

Case Serial Number: 10/800179

From: Barb O'Bryen

Location: Biotech-Chem Library

Remsen 1A69

Phone: 571-272-2518

barbara.obryen@uspto.gov

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STIC-Biotech/ChemLib

14/074

From:

Kosar, Andrew

Sent:

Wednesday, December 22, 2004 3:47 PM

To:

STIC-Biotech/ChemLib

Subject: sequence search 10/800,179

Please search SEQ ID NO:19 in Application 10/800,179.

The claim is drawn to proteins 'comprising' SEQ ID NO:19.

Thank you, Andrew Kosar

Andrew D. Kosar, Ph.D. Art Unit 1654 Office REMSEN 3C04 Mail REMSEN 3C18 (571)272-0913

DEC 22 2005

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Database
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
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                                                                                     US-10-800-179-19
4173
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	8	ID	Description
1	4173	100.0	780	۰,	ADK51951	Adk51951 Repeat
N	3448	٧.	884	N	AAR80341	
w	3448	•	884	N	AAW09213	
.4	3448	82.6	884	N	AAW53541	-
υ	3448	٠	884	N	AAW49728	
თ	3448	٠	884	w	AAY51882	
7	3448	٠	884	v	ABG31412	
œ	3448	82.6	884	7	ABW01628	
9	3296	79.0	2257	ш	AAP82961	
10	3296	79.0	2257	N	AAR41012	
11	3296	•	2257	N	AAW26347	
12	3296	•	2257	N	AAW53523	
13	3296	•	2257	w	AAY78282	
14	3296	79.0	2257	υı	ABG69272	
15	3296	•	2257	7	ADE44977	
16	3284	78.7	877	N	AAR80335	
17	3284	78.7	877	N	AAW49724	
18	3264		768	ຫ	ABP53466	
19	3253	78.0	832	N	AAR80252	
20	3253	78.0	832	ഗ	ABP53473	
21	3192		768	v	ABP53481	Abp53481 Protein
22	3182	76.3	988	N	AAR80253	
23	3182	76.3	988	S	ABP53474	
24	3176	76.1	1412	N	AAW53519	
25	3176					

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	
2998	3089	3089	3089	3089	3089	3089	3089	3158	3158	3158	3158	3158	3158	3158	3176	3176	3176	3176	
71.8	74.0	74.0	74.0	74.0	74.0	74.0	74.0	75.7	75.7	75.7	75.7	75.7	75.7	75.7	76.1	76.1	76.1	76.1	
1056	2107	2107	2107	2100	2025	2018	2018	2055	2055	2055	2055	2055	2055	2055	1465	1465	1464	1413	1
N	N	N	۲	ω	N	7	G	7	σ	w	N	N	N	۲	7	v	w	N	
AAR80254	AAW53521	AAW26345	AAP82959	AAY78280	AAR41010	ADE44975	ABG69270	ADE44976	ABG69271	AAY78281	AAW53522	AAW26346	AAR41011	AAP82960	ADE44969	ABG69268	AAY78278	AAW26343	
Aar80254	Aaw53521	Aaw26345	Aap82959	Aay78280	Aar41010	Ade44975	Abg69270	Ade44976	Abg69271	Aay78281	Aaw53522	Aaw26346	Aar41011	Aap82960	Ade44969	Abg69268	Aay78278	Aaw26343	
Polymer S	Amino aci	SELP1	SEPL1 pro	SELP1 ami	SELP1 mul	Recombina	Silk/Elas	Recombina	Silk/Elas	SELP2 ami	Amino aci	SELP2 syr	. SELP2 mul	SEPL2 pro	Recombina	Elas	EBSI	EBSI synt	

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ALIGNMENTS

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RESULT 1
ADK51951
ID ADK5
06-MAY-2004 (first entry)
                                                                                       WPI; 2004-023263/02.
                                                                                                 Kumar M;
                                                                                                                         20-MAY-2002; 2002US-0381913P
                                                                                                                                   20-MAY-2003; 2003WO-US015757.
                                                                                                                                              04-DEC-2003.
                                                                                                                                                       WO2003099465-A1
                                                                                                                                                                 Unidentified.
                                                                                                                                                                           repeat protein.
                                                                                                                                                                                    Repeat protein polymer repeat sequence, SEQ ID 19
                                                                                                                                                                                                         ADK51951;
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                                                                                                           (DOWO ) DOW CORNING CORP.
                                                                                                                                                                                                                  protein;
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Forming inorganic structure, for use as e.g. electronic photonic and nano composite materials, comprises providing substrate with repeat protein polymer, and exposing substrate to precursor containing inorganic

Claim 12; Page 8; 27pp; English.

The present invention relates to a method for forming an inorganic structure. The method comprises providing substrate with a repeat proteir polymer, and exposing the substrate to a precursor comprising inorganic species. The repeat protein polymer catalyzes the formation of an inorganic structure on the substrate. The repeat portion of the repeat protein polymer may be ADK51951-ADK51957, which may have a head sequence at the N-terminal end (ADK51958) and a tail sequence at the C-terminal end (ADK51958). protein

Sequence 780 AA;

Query Match

100.0%; Score 4173; DΒ 8 Length 780;

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RESULT 2
AAR80341
ID AAR8
XX AAR8
AC AAR8
XX Prot
XX Penc
XX Penc
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XX Penc
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XX Synt
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                                            Pendent group; repeating unit; enzyme recognition site; sealant; enzymatic cross-linking; biocompatible material; structural integmedical adhesive; wound closure; tissue repair; transglutaminase.
   WO9523611-A1
                       Synthetic
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Matches 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence of the protein polymer adhesion substrate (PPAS) SELP8K. The protein contains 12 repeats of the SELP8K monomer sequence (AAR80339). The protein can be used as a polymer substrate in an isopeptide cross-linking reaction catalysed by a transglutaminase enzymatic activity, e.g. Factor VIII or XIII. The polymers can be used in biological systems where in situ formation of a biocompatible material with structural integrity is required e.g. as medical adhesives and sealants or for wound closure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein polymers comprising repeating units and enzyme-catalysed covalent bond formation useful material for wound closure and tissue repair.
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Pred. No. 5.7e-217;
0; Mismatches 26;
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S 밁 Ş B S 밁 5

454

633 566 573 510 513 397 393 340 333 283

453

170

227 213

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RESULT 3
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                    Cappello
                                                                                                                                                                                                                                                                                                                /note= "Residue with functional group fo
837. .851
/note= "Elastin peptide repeat sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Silk fibroin peptide repeat sequence"
812. .831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Residue 69. .83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84. .97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide
                                                                                                                                                                                                                                                                                                                                                                                                          peptide repeat sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with functional group for crosslinking"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide (AAW09207, claim 4)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide repeat sequence"
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                                                                                                                                                                                                                                                                               repeat sequence"
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                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                               crosslinking"
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This SELPBK polymer sequence (mol.wt. 69,772) has been constructed from monomers composed of repeat units derived from silk fibroin (AAW09206) and elastin (AAW09207) (claim 4). The monomer (AAW09212) has been amplified by multicopy cloning in Escherichia coli (using plasmid pPT0345) to produce a recombinant protein polymer backbone with Lys functional groups for subsequent polyfunctional chemical crosslinking. The crosslinked polymer product forms a strongly adherent tissue adhesive or sealant. The polymer may be used to seal defects in vessel walls, e.g. artery, vein, capillary, lung, dura or colon, to increase tissue mass, or to produce biocompatible films for in vivo use. The sealants have the biocompatiblity of fibrin glues for in vivo use. The sealants have the biocompatible films for in vivo use. The sealants have the biocompatible films for in vivo use. The sealants have the biocompatible films for in vivo use. The sealants have the biocompatible films of the polymer product by recombinant methods, are easy to administer, and are gradually resorbed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue repair adhesive comprising polymer of structural protein repeat units - contg. hetero-atom functional gps. reactive with crosslinking agent, combines biocompatibility and high bonding strength.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 25; 103pp; English.
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Sequence 884 AA;

Length

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Best Local Similarity
Matches 752; Conserv 567 511 514 454 398 394 341 334 284 274 228 214 171 154 115 94 59 34 w GAGSGAGAGSGVGVPGVGVPGVGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGA GVGVPGKGVPGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGVGVPG VPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGV GAGSGAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVG PGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVGVP Conservative 82.6%; 90.6%; 0 Score 3448; DB 2; Pred. No. 5.7e-217; Mismatches Indels 52; Gaps 454 678 566 510 513 333 170 693 622 633 573 453 397 393 340 213 114 93 283 273 227 153

333 283 273 227

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                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 752
                                                                                                                                                                                                                                                                                                                                                                                                         This is the amino acid sequence of pPT0345 comprising the SELPBK protein, used in the method of invention, which involves the preparation of synthetic DNA sequence having repeating units from about 3-15 codons and encoding a protein of at least about 30 kDa. The method is useful for the production of high molecular weight polymers (e.g. synthetic silk), either nucleic acids or peptides that are the expression products of the nucleic acids and particularly high molecular weight peptides containing repeating units which are useful structural materials
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preparation of synthetic repetitive DNA - useful for construction large protein polymers having repeating units, used in structural material, e.g. synthetic silk.
                                                                                                                                                                                                                                                                                                                                                                     Sequence 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-193613/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ferrari
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high molecular '
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                                                                                                                                                                                                                                                                                                     Similarity
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                            standard;
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weight polymer; synthetic silk; silk worm
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                                                                                                                                                                                                                                                                          Score 3448; DB 2;
Pred. No. 5.7e-217;
0; Mismatches 26;
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12-OCT-1998
  Cappello J;
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                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                             SELP8K polymer.
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                                               (PROT-) PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                        r; SELP8K; silk-like protein; fibroin; elastin;
healing; transglutaminase; cross-linking.
                                                                                            94US-00205518
                                                                                                                                       95US-00397633
                                                  POLYMER TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
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CC SELPBK polymer is a synthetic silk-like protein comprising multiple CC copies of a monomer (see AAW49726) consisting of repeating units of silk-like sequences (CAGAS) and elastin-like sequences (VPGVG) including a CC reactive lysine residue. It was expressed in Escherichia coli from a CC plasmid ppT0345 as a 80 kDa protein. The SELPBK polymer was specifically CC designed to be functionalised with different reagents reactive to amines. CC claimed recombinant protein polymers are capable of covalent crosslinking by enzymatic reaction to form products which set quickly and have good CC dathed recombinant protein polymers are capable of covalent crosslinking by enzymatic reaction to form products which set quickly and have good CC adhesive properties and high strength. The proteins can comprise a CC repetitive maino acid backbone of repetitive units having collagen, CC fibroin, elastin or keratin motifs and at least 2 enzyme recognition CC sequences comprising a glutamine or lysine capable of enzyme catalysed CC isopeptide formation. The products can be used as medical adhesives and CC sealants, in the closure of wounds and repair of damaged tissue. (Updated CC on 25-MAR-2003 to correct PF field.)
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                                                                                                           VGVPGVGVPGVPGAGAGAGSGAGAGSGAGAGSGVGVPGVPGVPGVPGVPGVPGVPGK
                                                                                                                                                                                     PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVGVGVGVGVGKGVPGVG-PGVG-P
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90.6%;
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Pred. No. 5.7e-217;
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by enzymes, useful as medical a
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                                                                                                                       This invention describes a novel crosslinked protein composition (A) in which, before crosslinking, the protein (I) is new and comprises at least 70 wt. $ of repeating units GAGAGS (1) and GVGVP (2), and in at least two repeating units an amino acid (aa) is substituted by Lys or Arg to provide a Lys/Arg equivalent weight of 1-20 kD. (I) contains at least two as having a functional group reactive with at least one of aldebyde, iso(thio)cyanate and activated carboxy. (I) have similar biocompatibilty to fibrin glues, but set more quickly and give a bond with greater shear strength. They are made from readily available natural sources, are easy to administer and are gradually resorbed. This sequence represents a crosslinking protein polymer unit designated SELPBK
                                                                                                   Sequence 884 AA;
                                                                                                                                                                                                                                                                                                      Crosslinked protein composition, useful as tissue adhesive or sealant, comprises peptide repeating units that contain functional groups react with crosslinker.
                                                                                                                                                                                                                                                                               Example
                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Crosslinked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid pPT0345 protein fragment containing SELP8K polymer
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                                                    Conservative
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                                                 Score 3448; D. Pred. No. 5.7e 0; Mismatches
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                                                            3448; DB 3
No. 5.7e-21
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                                       Unidentified.
Synthetic.
                                                                              protein polymer; functional group; crosslink; sealing; filling; tissue; tissue mass; tissue bonding; resorbable bond; flexible bond; sealant; adhesive; wound healing; burn dressing; blood flow; ruptured vessel; artery; vein; structural protein; vulnerary; fibroin; elastin; collagen
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to protein polymers having repetitive units from naturally occurring structural proteins such as fibroin, elastin, collagen and keratin. The polymers comprise a functional group which can be chemically crosslinked with appropriate crosslinkers. The protein polymer is produced by recombinant DNA technology. The protein polymer is useful for sealing or filling a defect in viable tissue, particularly for augmenting tissue mass. The protein polymer is useful in a variety of applications related to their physical, chemical and biological properties, and/or to bond together separated tissue to provide a stable, flexible or resorbable bond. The protein is particularly useful as a sealant or adhesive, in wound healing or as a burn dressing e.g. to stop or staunch the flow of fluid (e.g. blood) through ruptured vessels (e.g. arteries or veins). The present sequence represents SELP8K polymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crosslinked protein composition used as sealant or adhesive for sealing or filling defect in viable tissue, as burn dressing, or in wound healing e.g. to staunch flow of fluid e.g. blood, through ruptured vessels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2;
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02-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                  VG-PGVG-
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   G-PGVG-PGVG-
                                                                                             GSGAGAGSGAGAGSGVGVPGVGVPGVGVPGVGVPGVG-PGVG-PGVG-PGAGAGS
                                                                                                                                                                                                                                                                                                                                         GVGVPGVGV
                                                                                                                        PGVGVPGAGA
                                                                                                                                                                                                         GSGAGAGSGAGAGSGVGVPGVGVPGVGVPGVGVPGKGVPGVGVPGVGVPGAGAGAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Col 17; 46pp; English.
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96US-00642246.
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                                                        -PGVG-
                                                                                 , GSGAGAGSGAGAGSGVGVPGVGVPGV
            1-PGVG-
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90.6%;
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            - PGAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGVPGKG
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Pred. No. 5.7e
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217;
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Matches 752
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02-MAY-1996;
29-NOV-1999;
                                                                                                                                                                                                                                WPI;
                                                                           Sequence 884
                                                                                             The present invention relates to crosslinked protein composition. The invention is useful as sealants or depots to provide for relatively uniform release of a physiologically active product e.g., drug and for the formation of articles of manufacture such as gels, films, threads, coatings. The present sequence is plasmid pPTO345 SELPBK polymer proteins.
                                                                                                                                                                                    Crosslinked protein composition useful as sealing a defect in tissue, protein prior to crosslinking comprises repetitive units of 3-15 amino acids of natural structural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABW01628
                                                                                                                                                                 Example
                                                                                                                                                                                                                                                                                                                                           05-APR-2002; 2002US-00117931
                                                                                                                                                                                                                                                                                                                                                                 05-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                      US2003104589-A1
                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                 coating; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Crosslinked
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid pPTO345 SELP8K polymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-FEB-2004
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                                 il Similarity
752; Conser
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standard;
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ilarity 90.6%;
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96US-00642246.
99US-00451206.
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                               ; Score 3448; Di
; Pred. No. 5.7e
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                               DB 7;
5.7e-217;
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GVGVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGVGVPG
                                                                VPGVG-PGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGV
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                                             PGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVGVP
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ARSULT 9
AAP82961
ID AAP8
XX AAP8
AC AAP8
AC AAP8
DT 25-M
DT 27-N
XX SEPL
XX Repe
XW SELF
XX SUNT
XX SUNT
XX SPI
X
      Key
Region
                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                               Repeat unit; collagen; keratin; immunisation; monom SELP3; pSY1397; Bombyx mori; silk fibroin; elastin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEPL3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
27-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprising gagags of silk fibroin and
      Location/Qualifiers 38. .49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2257
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                                                                                                                                                                                   The SELP3 sequence present in pSY1377 encodes a protein of MM168,535. The repeating unit gagags is found in naturally occuring silk fibroin protein. Silk-like proteins mimic the composition and physical properties of silk of Bombyx mori. The repeating unit group is found in naturally occuring elastin The protein mimics the properties of elastin and provides for elastineries. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                   Disclosure; Page ?;
                                                                                                                                                                                                                                                                                                                                        04-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                        29-OCT-1987;
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                                                                       ding oligopeptide ı
collagen, keratin
         Conservative
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/note= "vpgvg"
2202. .2231
/label= ren-
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/label= repeat unit
/note= "gagags found in natural
                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= repeat_region
/note= "gagags"
2161. .2201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
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/note= "vpgvg found
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/note= "vpgvg"
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/note= "(gvgvp)8 (gaga
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/note= "gagags"
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n or peptide(s)
                                                                                                                                     0;
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                                                                                                                                     Score 3296; DB 1;
Pred. No. 8.8e-207;
0; Mismatches 25;
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for immunisation.

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                                                                                                                                                    Length
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                                                  -GPGAGAGSGAGAGSGAGA
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RESULT 10
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ID AAR41
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AC AAR41
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10-MAR-1994
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                 SELP3
                                                                       AAR41012 standard;
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                multimeric protein.
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protein; elastic
                                (revised)
(first en
                                                                       protein;
                                entry)
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properties; elastin-like protein;
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                                                                                                                                                                                                                                                      -GPGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVG
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                                                                                                                                                                                                                                                          Sequence 2257 AA;
                                                                                                                                                                                                                                                                      The SELP3 multimeric protein contains the (GAGAGS)n motif typical of silk -like proteins (see AAR41006 and AAR41007) as well as the (GVGVP)n motif typical of elastin-like proteins (see AAR41009). The synthetic DNA coding sequence for SELP3 was constructed by self-ligation of sticky-ended momommer coding sequences. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                     DNA compsn. encoding peptide contg. oligopeptide repeating unit(s) provides efficient prodn. of e.g. silk-like protein(s) elastin-like proteins and antigens for immunisation.
                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                     Ferrari FA,
Capello J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       silk-like protein; Bombyx mori; fibroin; mimic; oligomeric peptide; repetitive peptide sequence.
                                                                                                                                                                                                                                                                                                                      Example 5; Page 32 (Column 41); 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            29-OCT-1987;
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Crissman JW;
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/label= repeat region
/note=_"[(GVGVP)8-(GAGAGS)8]24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= repeat_unit
note= "-(GVGVP)8-(GAGAGS)8-"
                                                                       . 137
                                                                                                                                                                                                                        Score 3296; DB 2;
Pred. No. 8.8e-207;
0; Mismatches 25;
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04-NOV-1986;
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20-NOV-1997
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                                       24-JUN-1997
                                                                                                    SELP3 synthetic elastomeric protein
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87US-00114618
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                                                                                   SELP3; protein polymer; elastin; fibroin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthetic double-stranded oligonucleotides are annealed to form a 'monomeric' gene, the monomers are assembled into multimers and these are cloned into vectors to allow production of the high mol.wt. protein in host (preferably) E. coli cells. The general method allows production of fibrous or structural proteins, including crystalline, elastomeric, tough and bony materials such as those that mimic (and can substitute for) silk, elastin, collagen, keratin etc. The properties of the protein can be controlled by varying the type of units in the monomer, the number of units per multimer, the spacing between them and the number of multimer repeats. (Updated on 25-MAR-2003 to correct PF field.)
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06-NOV-1990;
22-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Col 45; 90pp;
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90US-00609716.
93US-00053049.
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Pred. No. 8.8e-207;
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Preparation of synthetic repetitive DNA - useful for construction large protein polymers having repeating units, used in structural material, e.g. synthetic silk.
                                                                                                                                                                                                                                                                                        Synthetic oligonucleotide; peptide repeat unit; DNA repeat unit; high molecular weight polymer; synthetic silk; silk worm.
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29-OCT-1987;
22-APR-1993;
29-DEC-1993;
                    The present invention describes a recombinantly produced protein (I) of 30 to 250 kilodaltons (kDa), where 50% of the protein is comprised of at least 1 repeating unit of a naturally occurring protein. The proteins comprising repeating units may be used as fibrous or structural proteins, including crystalline, elastcomeric, tough and bony materials e.g. proteins sintlar to but different from, silk, elastin, collagen, keratin or other naturally occurring structural polymers having repetitive amino acid sequence motifs. The proteins may have the capability of forming or participating in the formation objects such as films, fibres, gels, membranes or may be amorphous, such as in adhesives, coatings, viscous
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structure; film; gel; membrane;
viscous fluid; emulsion; crystal
elastin; collagen; keratin.
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87US-00114618.
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amorphous; adhesive; coating;
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GAGAGSGAGAGSGVGVPGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGV----

Query Match Best Local S Matches 755

Similarity

79.0%;

Score 3296; DI Pred. No. 8.8e 0; Mismatches

1.8e-207; 1es 25;

Indels 340;

Gaps

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ВB 5

Length

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Conservative

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29-OCT-1987;
22-APR-1993;
29-DEC-1993;
07-JUN-1995;
                                   The invention relates to a recombinantly produced protein of 30-250 kD comprises at least 50% (by number of amino acids (aa)) of a naturally occurring repeat unit, of 3-20 aa, from a naturally occurring structura protein (especially silk fibroin and elastin, also collagen and fibronectin (FCB)). The recombinant proteins are useful, e.g. as structural components of prosthetic devices or synthetic fibres. The physical properties of the protein can be adjusted by varying the combination of repeat units, and the protein may retain the properties natural proteins while also having additional properties. The present sequence is a recombinant protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ferrari F
Cappello
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Synthetic.
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29-OCT-1987;
22-APR-1993;
29-DEC-1993;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a novel recombinant protein (1) of at least 30 kDa comprising at least 50 percent of amino acids of at least one naturally occurring repeating unit of a naturally occurring structural protein, where a repeating unit comprises 3-20 amino acids, and where each of the same repeating unit comprises the same amino acids. (1) has a variety of uses including use as structural component of e.g. prosthetic devices and synthetic fibers. The protein has the properties of a naturally occurring structural protein but can be modified to have new properties. This sequence represents SELP3, a recombinant structural protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2257
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745 GVPGKGVPGVG-PGVG-PGVG-PGVG-PGAGAGSGAGAGS 780	707	653 GSGAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGVPGVGVP	621 VPGVGVPGKGVPGVG-PGVG-PGVG-PGV	586 V	529 GAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGVPG	497 PGVGVPGVGVPGKGVPGVG-PGVG-PGVGP	463 G-PGV	407GPGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGV	373 GVGVPGVGVGVGVGVGKGVPGVG-PGVG-PGVG-PGV	340 -PGVG-PGV	287GPGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVGVGVGVPGVGVP	249 GAGSGYGYPGYGYPGYGYPGXGYPGYG-PGYG-PGYG-PGY	216 PGVG-PGVG-PGV	167GPGAGAGSGAGAGSGAGAGSGAGAGSGYGVPGYGYPGYGVPGYGYPGYG- 	
	GV 744 GV 1117	706 VP 1057	GA 652 GA 997	VG 620 VG 937	PG 585 	GP 528 GS 817	GV 496 - 757	GV 462 GV 697	406 GA 637	GS 372 - GS 577	VG 339 VG 517	286 GA 457	GA 248 GA 397	G- 215 GV 337	GS 277

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Search completed: December 30, 2004, 12:57:43 Job time : 172 secs

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Blochemistry 26, 1497-1503, 1987
A;Title: Repeating structure of chick tropoelastin revealed by complementary DNA cloning A;Reference number: A26601; MUID:87242320; PMID:3593675
A;Accession: A26601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N;Alternate names: tropoelastin C;Species: Gallus gallus (chicken) C;Species: Gallus gallus (chicken) C;Date: 05-Oct-1988 #sequence revision 26-Jul-1996 #text_change 09-Jul-2004 C;Accession: A26601; A30795; A27264
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ALIGNMENTS

chicken (fragment)

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A;Molecule type: mRNA
A;Residues: 85-784 <BAU>
A;Residues: 85-784 <BAU>
A;Residues: 85-784 <BAU>
A;Residues: 85-784 <BAU>
A;Cross-references: GB:M21880; NID:g212741; PIDN:AAA49082.1; PID:g212742
A;Cross-references: GB:M21880; Nibhikawa, T.; Tajima, M.; Fukasawa, T.
A;Chinitsu, I.; Tajima, S.; Nishikawa, T.; Tajima, M.; Fukasawa, T.
A;Chinitsu, I.; Tajima, S.; Nishikawa, T.; Tajima, M.; Fukasawa, T.
A;Title: Sequence analysis of elastin cDNA from chick aorta and tissue-specific transcri
A;Reference number: A27264; MUID:87297534; PMID:3502711
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A;Residues: 1-212,237-54,535-784 <BR2>
A;Residues: 1-212,237-544,535-784 <BR2>
A;Cross-references: UNIPROT:P07916; GB:M15889; NID:g212803; PIDN:AAA49108.1; PID:g212804
A;Baule, V.J.; Foster, J.A.
Biochem. Biophys. Res. Commun. 154, 1054-1060, 1988
Biochem. Biophys. Res. Commun. 154, 1054-1060, 1988
A;Title: Multiple chick tropoelastin mRNAs.
A;Reference number: A30795; MUID:88309083; PMID:2841924
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A;Residues: 491-569,'G',571-604,'A',606-643,'A',645-687,'R',689-700,'R',702-784 <TOK>
A;Cross-references: GB:M18633; NID:g211742; PIDN:AAA48761.1; PID:g211743
C;Superfamily: elastin
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                                                                                                                                                                                                                                                                                                                 9 LPGVLLLFSILPASQQGGVPG-AIPGGGVP-----GGGFFPGAGVG-----GLGA
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AAKAGAGLGGVGG1GGLGGVGGVGVPGGLGVPGVVQPGVGAAGKPPKVPGAG1PGAFPGG
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EAMS
elastin precursor - mouse
elastin precursor - mouse
N;Alternate names: tropoelastin
C;Species: Mus musculus (house mouse)
C;Accession: A55721
R;Wydner, K.S.; Sechler, J.L.; Boyd, C.D.; Passmore, H.C.
Genomics 23, 125-131, 1994
A;Title: Use of an intron length polymorphism to localize the tropoe
A;Reference number: A55721; MUID:95130069; PMID:7829060
A;Recule type: mRNA
A;Residues: 1-860 < WYD>
A;Cross-references: UNIPROT:P54320; GB:U08210; NID:g473273; PIDN:AAJ
C;Genetics:
A;Map position: 5
C;Superfamily: elastin
C;Keywords: alternative splicing; extracellular matrix; glycoprotein
F;1-27/Domain: signal sequence #status predicted <MAT>
F;28-860/Product: elastin #status predicted
F;850-855/Disulfide bonds: #status predicted
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Best Local S
Matches 383
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VLGARPFPGGGVAARPGFGLSPIYPGGGAG-GLGVG
                         VPGVGPGVGPGVG---PGVG----PGAGAGSGAGAG
                                                                          VPGRVAGAAP
                                                                                                                           G-PGVGPGVG-PGAGAGS--GAGAGSGA---GAGSGAGAGSGVGVP-GVGVPGVGVBKG
                                                                                                                                                                                                                            G--AGAGSGAGAGSGAGAGS----GAGAGSGVGVPGVGVPGVGVP----GKGVPGVGPGV
                                                                                                                                                                                                                                                           PAAAAAAAAKAAKAGLGPGVGGVPG-
                                                                                                                                                                                                                                                                         GSGAGAGSGAGAGSGAGAGSGV-GVPGVGVPGVGVP-GKGVPGVGPGVGPG--VGPGVGP
                                                                                                                                                                                                                                                                                                                                   GAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGVPGVGVGPGVGPGVGPGVG--
                                                                                                                                                                                                                                                                                                                                                            PAAAAKAAKAAKYGARGGVGIPTYGV-GAG----GFPGYGVGAGAGLG-GASPAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                GAGAGSGAGAGSGVGVPGVGVPGVGVPGVGPGVGPGVGPGVGPGVGPGAGAGS
                                                                                                                                                                                                                                                                                                                                                                                                                              AGSGA--GAGSGV--GVPGVGVPGVGVPG-KGVPGVG--PGV-GPGVG-GPGVGPGAGAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAAKAAKYGAGGAGV-LPGVG--GGGIPG----
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                                                                                                                                                                                                        GGLGGAGSPAAAKSAAKAAAKAQYRAAAGLGAGVPGFGA-GAGVPGFGAGAGVPGFGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                <u>AAKAAKYGAAGGLVPGGPGVRLPGAGIPGVGGIPGVGGIPGVGGPGIGGPGIVGGPGAVS</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGPFGGQQPGVPLGYPIKAPKLPGGYGLPYTNGKLPYGVA-GAGGKAGYPTGTGVGSQAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQPGGVPGAVPG-GLPG-GVPGGVYYPGAGIGGLGGGGGALGPGGKPPKPGAGLLGTFGA
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                                                  GLGAG
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Pred. No. 5.9e-66;
0; Mismatches 274
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                                                  LGAG-
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                                                  GLGAGGGVSPAAAAKAAKYGAAGLG----
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elastin precursor - rat

N;Alternate names: tropoelastin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jan-1991 #sequence revision 16-Aug-1996 #text change 09-Jul-2004
C;Accession: A36166; A30878; A36523; S02173; I54172; I68505
R;Pierce, R.A.; Deak, S.B.; Stolle, C.A.; Boyd, C.D.
                                                                                                                                                                                                     RESULT
EART
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A.Note: the list of introns may we accept.

A.Note: the list of introns may we accept.

C.Superfamily: elastin
C.Keywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F.1-21/Domain: signal sequence #status predicted <SIG>
F.1-21/Domain: signal sequence #status predicted <MAT>
F.22-864/Product: elastin #status predicted <MAT>
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R;Pierce, R.A.; Alatawi, A.; Deak, S.B.; Boyd, C.D.
Genomics 12, 651-658, 1992
A;Title: Elements of the rat tropoelastin gene associate
A;Reference number: I54172; MUID:92241859; PMID:1572637
A;Accession: I54172
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A;Cross-references: GB:004035; NID:g207442; PIDN:AAA42268.1; PID:g207443
A;Cross-references: GB:004035; NID:g207442; PIDN:AAA42268.1; PID:g207443
R;Franzblau, C.; Pratt, C.A.; Faris, B.; Colannino, N.M.; Offner, G.D.; Mogayzel J.J. Biol. Chem. 264, 15115-15119, 1989
J. Biol. Chem. 264, 15115-15119, 1989
A;Title: Role of tropoelastin fragmentation in elastogenesis in rat smooth muscle A;Reference number: A36523; MUID:89359327; PMID:2768256
A;Accession: A36523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:099372; GB:M60647; GB:J05292; NID:g207444; R;Deak, S.B.; Pierce, R.A.; Belsky, S.A.; Riley, D.J.; Boyd, C.D. J. Biol. Chem. 263, 13504-13507, 1988
A;Title: Rat tropoelastin is synthesized from a 3.5-kilobase mRNA. A;Reference number: A30878; MUID:88330868; PMID:2971041
A;Accession: A30878
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A;Title: Heterogeneity of rat try
A;Reference number: A36106; MUID
A;Accession: A36106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 558-864 < RE2 >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 264-533 <RES>
A;Cross-references: GB:M86372; NID:g207455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arch. Biochem. Biophys. 268, 551-558, 1989
A;Title: Characterization of rat heart tropoelastin.
A;Reference number: S02173; MUID:89117149; PMID:2913947
A;Accession: S02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M86376; NID:g207459; PIDN:AAA42272.1; PID:g207462
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A;Molecule type: DNA
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A;Residues: 'IP',369-545,548-764,770-864 <RIC>
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A; Residues: 1-864 < PI
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                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                          Matches
                           162
                                                                     140
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                                                                                                                                                                                                                                                                                                                                                               Similarity
VGPGVG---PGAGAGSGAGAGSGAGAGS-SGAGAGSGVGVPGVGVPGVGVPG--KGVPGVG
                                                                   VPGAVGVGGVPGAVGGIGGIGGLGVSTGAVVPQLGAGVGAGGKPGK-VPGVGLPGVYPGG
                                                                                                 GPGA-GAGSGAGAGSGAGAGSGAGAGSGVGVP--GVGVPGVGVPGKGVPGVG-PGVGP-G
                                                                                                                                                            PGGLGGAGPGAGLSYASRPGGVLVPGGGAGAAAAYKAAAKAGAGLGGIG-GVPGGVGVGG
                                                                                                                                                                                                        AGSGAGAGSGAGAGSGVGVPGVGVPGVGV---
                                                                                                                                                                                                                                               GVPGAVPGGVPG-GLPG-GVPGGVYYPGAGIGGGLGGGALGPGGKPPKPGAGLLGAFGAG
                                                                                                                                                                                                                                                                                            GVPGV---GVPGVGVPGKGVPG----VGPGVGPGVGPG-VGPGA----GAG----SGAG
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                          28.48;
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                                                                                                                                                                                                                                                                                                                                                             Score 1185;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene associated with alternative
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                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                        299;
                                                                                                                                                                                                   -----PGKGVPGVGPGVGPGV 106
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                                                                                                                                                                                                                                                                                                                                                                                  Length 864;
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                                                                                                                                                                                                                                                                                                                                        140;
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EABO
                                     A;Molecule type: mRNA
A;Residues: 1,'RS',4-11,'E',13-636,'V',638-747 <RAJ>
A;Cross-references: GB:J02717; NID:g163019; PIDN:AAA30503.1; PID:g163020
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                                                                                GAG-GVIPGAVGLGGVSPAAAAKAAKYGAAGLG-GVLGARPFPGGGVAARPGFGLSPIYP
                                                                                                                     GVGPGVGPGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGV-GVPGVGV---PGKGVPGVGP
                                                                                                                                                             GVPGGVAGGAPAAAAAAKAAAKAAQYGLGGAGGLGAGGLGAGGLGAGGLGAG-GL
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N;Contains: elastin precursor, splice form b; elastin precursor, splice form c C;Species: Bos primigenius taurus (cattle) C;Apace: 08-Uun-1989 #sequence revision 26-Uul-1996 #text_change 09-Uul-2004 C;Accession: A31865; A26728; B26728; C26728; A22343; I45886 R;Yeh, H.; Anderson, N.; Ornstein-Goldstein, N.; Bashir, M.M.; Rosenbloom, J.C.; Abram Biochemistry 28, 2365-2370, 1989 A;Title: Structure of the bovine elastin gene and S1 nuclease analysis of alternative A;Reference number: A31865; MUID:89274159; PMID:2543440 A;Accession: A31865 A;Molecule type: DNA
A;Residues: 1-27 <XEH-,
A;Cross-references: UNIPROT:P04985; UNIPROT:Q28101; GB:J
A;Cross-references: UNIPROT:P04985; UNIPROT:Q28101; GB:J
A;Raju, K.; Anwar, R.A.
J. Biol. Chem. 262, 5755-5762, 1987
J. Biol. Chem. 262, 5755-5762, 1987
A;Title: Primary structures of bovine elastin a, b, and A;Reference number: A92640; MUID:87194772; PMID:3032943
A;Accession: A26728 elastin precursor, splice form a - bovine N,Alternate names: tropoelastin GB:J02855; deduced NID: 9340504; from the sequences PIDN:AAA3077 Abrams

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of.

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C;Superfamily: elastin

C;Reywords: alternative splicing; extracellular matrix; glycoprotein; hydroxylysine
F;1-747/Product: elastin precursor, splice form a #status predicted <EPA>
F;1-225,260-747/Product: elastin precursor, splice form c #status predicted <EPC>
F;1-225,240-747/Product: elastin precursor, splice form b #status predicted <EPB>
F;1-26/Domain: signal sequence #status predicted <SIG>
F;1-747/Product: elastin #status predicted <SIG>
F;27-747/Product: elastin #status predicted <ANT>
F;105,109,252,271,275,324,327,400,404,407,445,448,489,493,544,548,552,606,609,645,649,68
F;737-742/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 678-683,685-747 <ROS>
A;Cross-references: GB:M31898; NID:g163015; PIDN:AAA96417.1; P
A;Cross-references: GB:M31898; NID:g163015; PIDN:AAA96417.1; P
R;Brown, P.L.; Mecham, L.; Tisdale, C.; Mecham, R.P.
Biochem. Biophys. Res. Commun. 186, 549-555, 1992
A;Title: The cysteine residues in the carboxy terminal domain
A;Reference number: A58621; MUID:9237651; PMID:1632791
A;Contents: annotation, disulfide bonds
C;Comment: The term tropoelastin refers to a soluble precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Rosenbloom, J.

Lab. Invest. 51, 605-623, 1984

A;Title: Biology of disease: Elastin: Relation of protein A;Reference number: I45885; MUID:85059254; PMID:6150137

A;Accession: I45886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1, 'RS', 4-11, 'E', 13-225, 260-636, 'V', 638-747 <RA3>
A; Residues: 1, 'RS', 4-11, 'E', 13-225, 260-636, 'V', 638-747 <RA3>
A; Cross-references: GB: K03506; NID:g163027; PIDN:AAA30506.1; PID:g163028
A; Cicila, G.; May, M.; Ornstein-Goldstein, N.; Indik, Z.; Morrow, S.; Yel
Biochemistry 24, 3075-3080, 1985
B; Title: Structure of the 3' portion of the bovine elastin gene.
A; Title: Structure of the 3' portion of the bovine elastin gene.
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A;Cross-references: GB:K03505; NID:g163025; PIDN:AAA30505.1; PID:g163026
A;Accession: C26728
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A; Residues: 613-747 < CIC>
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                                                                                                  PTGAGVKPKAQVGAGAFA---
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ons is incomplete
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GKSCG
                                           GSGAG
                                                                                        FGAAGLGGVLGAGQPFPIGGGAG---
                                                                                                                                 GSGAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGVPGVGPGVGPGVGPGVGPGVGPGAGA
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C;Species: Ovis orientalis aries, Ovis ammon aries C;Date: 23-Aug-1996 #sequence revision 13-Mar-1997 C;Accession: S59623; A24758 R;Mauch, J.C.; Sandberg, L.B.; Roos, P.J.; Jimenez, Matrix Biol. 14, 635-641 1994 R;Yoon, K.; Davidson, J.M.; Boyd, C.; May, Arch. Biochem. Biophys. 241, 684-691, 1985 A;Title: Analysis of the 3' region of the EA;Reference number: A24758; MUID:85305763; C;Keywords: alternative splicing; extracellular matrix; F;760-765/Disulfide bonds: #status predicted A; Molecule type: mRNA A; Residues: 655-669, 671-716, 732-770 A; Molecule type: mRNA A; Residues: 1-770 < MAU> A; Accession: A24758 A; Status: preliminary; not compared A; Accession: S59623 A; Reference number: S59623 A; Title: Extensive alternate exon Cross-references: UNIPROT: P11547 Superfamily: elastin Similarity GSGAGAGSGVGVP-GVGVPGVGVPGKGVPGVGPGV---GPGVGPGVGPGAGA-GSGA--sheep Conservative 27.5%; 41; Score 1146.5; Pred. No. 9.5 usage with *005 P.J.; Jimenez, Mismatches at conceptual sheep elastin ; PMID:3839997 M.; LuValle, the ń 239; BB end (domestic sheep)
#text_change 09-Jul-2004 F) . ; translation of the Indels Length glycoprotein; Christiano, P.; Ornstein-Goldstein, N.; gheep 217; A.M.; Deak, Gaps hydroxylysine Smiti

85

101

GVGGLGVSTGAVVPQLGAG

143

-6

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period clock protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar
C;Accession: A24403
R;Shin, H.S.; Bargiello, T.A.; Clark, B.T.; J
Nature 317, 445-448, 1985
A;Title: An unusual coding sequence from a Dr
A;Reference number: A24403; MUID:86014384; PM
A;Accession: A24403
A;Cross-references: UNIPROT:P08399; GB:X02966; GB:M12039; NID:g55125; PIDN:CAA26710.1; EC;Comment: Mutations within the per locus of the fruit fly affect a variety of natural blogous locus with multiple tandem repeats of nucleic acid hexamers (ACNGGN, TCAGGC) that C;Comment: The serine residues of the S-G repeats found in certain proteoglycans are att C;Superfamily: period clock protein; EGF homology C;Keywords: circadian rhythm; tandem repeat
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UMMS
                                                                                         A; Molecule type: DNA
A; Residues: 1-713 <SHI>
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Pred. No. 3.3e
64; Mismatches
                                  -GTATATGTGTGTGTGTGTGTGTGTDTSTGT
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3e-61;
                                                                     GTGLGSGSGSGSGTGTGTGT
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RESULT 7
F70806
F70806
hypothetical glycine-rich protein Rv3508 - Mycobacterium tuberculosis C; Species: Mycobacterium tuberculosis C; Species: Mycobacterium tuberculosis C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09: C; Accession: F70806
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Ha Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Nature 393, S37-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Ba A; Fulle: Deciphering the biology of Mycobacterium tuberculosis from A; Reference number: A70500; MUID:98295987; PMID:9634230
A; Accession: F70806
A; Status: preliminary; nucleic acid sequence not shown; translation Mycobacterium tuberculosis translation S.; Barrell, sis from the c , C.; Harris, D. S.; Hamlin, N.; , S.; Squares, S not (strain 1, B.G. complete D., Ø Holroyd, Gordon,

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A;Molecule type: DNA
A;Residues: 1-1901 <COL>
A;Residues: 1-1901 <COL>
A;Cross-references: UNIPROT:053553; GB:AL022022; GB:AL123456; NID:g3261554; PIDN:CAA1774
A;Experimental source: strain H37Rv
C;Genetics:
C;Genetics:
A;Gene: Rv3508
A;Gene: Rv3508
C;Superfamily: collagen alpha 1(IV) chain
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                                                                   AGGAGGAGDNNFNGGQGGAGGQGGQGGLGGASTTSINANGGAGGNGGTGGKGGAGGAGTL
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RESULT 8
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C;Species Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: B70807
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon R;Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genc A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70807
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-1079 cOL>
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A;Cross-references: GB:AL022022; GB:AL123456; NID:g3261554; PIDN:CAA17749.1;
A;Experimental source: strain H37Rv
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C; Superfamily:
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A;Cross-references: GB:AL022022; GB:AL123456; NID:g3261554;
A;Experimental source: strain H37Rv
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                                       VGVPGVGVPGVGVPGKGVPGVGPGVGPGVGPGVGPGAGAGSG--AGAGSGAGAGSGAGAG 371
                                                                                GGTGGVGGTGGDGGNAGTGAGDPGKG-GTGGTGGTGGSGGAGGSGGANFNGGTGGTGGTG
                                                                                                                                                                 DQPGATGGTGFAGGAGGAGGSGGSSCAGGTNGSGGAGGTCGQVVAGGAGISFSNGSNGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----SGAGAGSGAGA-----
                                                                                                                                                                                                          -----AGAGSGVGVPGVPGV-----
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AATGVGDGGDGGNG-GNGGNGGTGVGSPGGLGGAGGGTGGLGGAGAGGGA
                                      <u>AGSGVGVPGVGVPGVGVPGVGPGVGPGVGPGAGAGAGSGAGA</u>
                                                                              PGGDGGNAGVGGKGGTNGNGGSGGTGGTGGPGGSGGAPTGSGTGGKGGAGGDGGDGADGG
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elastin precursor, long splice form - human

N;Alternate names: tropoelastin

C;Species: Homo sapiens (man)

C;Date: 22-Uun-1990 #sequence revision 26-Jul-1996 #text_change 09-Jul-2004

C;Accession: A32707; A33705; A30524; A53891

R;Indik, Z; Yeh, H; Ornstein-Goldstein, N; Sheppard, P; Anderson, N; Rosent

Proc. Natl Acad. Sci. U.S.A. 84, 5680-5684, 1987

A;Title: Alternative splicing of human elastin mRNA indicated by sequence analyse
A;Reference number: A32707; MUID:87289668; PMID:3039501

A;Accession: A32707

A;Molecule type: mRNA
A;Residues: 1-500,507-792 <IND>
A;Cross-references: UNIPROT:P15502; UNIPROT:QSUMK5; GB:M16983; GB:J02948
A;Cross-references: UNIPROT:P15502; UNIPROT:QSUMK5; GB:M16983; GB:J02948
A;Cross-references: UNIPROT:P15502; UNIPROT:QSUMK5; GB:M16983; GB:J02948
A;Bashix, M.M.; Indik, Z; Yeh, H.; Ornstein-Goldstein, N.; Rosenbloom, J.C.; Ab
J. Biol. Chem. 264, 8887-8891, 1989

A;Title: Characterization of the complete human elastin gene. Delineation of unu
A;Reference number: A33705; MUID:89255358; PMID:2722804

A;Residues: 1-27 <BAS>
A;Residues: 1-27 <BAS>
A;Cross-references: GB:J04821; NID:g182052; PIDN:AAA52379.1; PID:g553276
A;Cross-references: GB:J04821; NID:g182052; PIDN:AAA52379.1; PID:g553276
A;Title: Cloning of full-length elastin cDNAs from a human skin fibroblast recom
A;Reference number: A30524; MUID:89009960; PMID:3171221

A:Accession: A30524; MUID:89009960; PMID:3171221 A;Accession: A30524
A;Modecule type: mENA
A;Residues: 1-453,483-617,651-792 <FAZ>
A;Cross-references: EMBL;M36860; NID:g182061; PIDN:AAA52382.1; PID:g182062
A;Cross-references: EMBL;M36860; NID:g182061; PIDN:AAA52382.1; PID:g182062
A;Note: this sequence represents a composite of several splice forms
A;Fazio, M.J.; Olsen, D.R.; Kuivaniemi, H.; Chu, M.L.; Davidson, J.M.; Rose
A;Title: Isolation and characterization of human elastin cDNAs, and age-ass
A;Reference number: A53891; MUID:88156138; PMID:2831431
A;Accession: A53891
A;Holecule type: mENA
A;Residues: 164-453,483-500,507-617,651-792 <FAZ> RESULT 10 EAHU PID:g553276 , Z.; Ornstein-Goldstein, and age-associated fibroblast recombinant J.M.; Rosenbloom, sequence analysis J.C.; of unusual Rosenbloom, Abrams,

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A;Map position: 7q11.23-7q11.23
(;Superfamily: elastin
C;Keywords: alternative splicing; extracellular matrix;
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-792/Product: elastin #status predicted <MAT>
F;782-787/Disulfide bonds: #status predicted
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A; Gene: GDB: ELN
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A;Map position: 7q11.23-7q11.23
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                                        VGVPGVGVPGVGPGKGVPGVGPGVGPGVGPGAGAGSGAGAG
                                                                                                       VPG-VGVPGVGVPGVGPGVGPGVGPGVGPGAGAGSGAGAGSGAGAGSGAGAGSG-
                                                                                                                                                                                              VGVAPGVGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLRAAAGLGAGIPGLGV-GVGV
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                 VGAAGLG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.3%; Score 1055.5; DB 1;
40.6%; Pred. No. 2.4e-56;
tive 47; Mismatches 281;
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A; Residues: 1-718 < XUA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                   AGAGSGAGAGSGAGAGSGVGVPGVGVFGVGVPGKGVPGVGPGVGPGVGPGVGPGAGAGSG
                                                                                                                       AAAAAAVGAGQEGIRGQGAGQGGYG-
                                                                                                                                                  SGAGAGSGAG----AGSGVGVPGVGVPGVGVPGVGVPGVGPGVGPGVGPGAGAGSG
                                                                                                                                                                                                               GAGAGSGAGAGSGVGVPGVGVPGVGVPGVGVPGVGPGVGPGVGPGVG-PGAGAGSGAGAG
                                                                                                                                                                                                                                                                           GAGAGSGAGAGSGVGVPGVGVPGVGVPGKGVPGVGPGVGPGVGPGVGPGAGAGSGAGAGS
                                                                                                                                                                                                                                                                                                    AAAGGAGQGGYGGLGSQGAGRGGLG--GQGAGAVAAAAAGGAGQG-GYGGLGSQGAGRG-
                                                                                                                                                                                                                                                                                                                                  GAGAGSGAGAGSGVGVPGVGVPGVGVPGVGVPGVGPGVGPGVGPGAGAGSGAGAGS
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                                                                                                                                                                                                                                                                                                                                                                                               GAGAGSGAGAGSGVGVPGVGVPGVGVPGVGVPGVGPGVGPGVGPGVGPGAGAGSGAGAGS
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AGAAAAAAGGAGQGGYGGLGGQGVGRGGLGGQGAGAAAAG-GAGQGGYGGVGSGASAASA
                          AGQGGLGGQGAGQGAGAAAAAAG-GVRQGGYGGLGSQGAGRG
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                                                                                                                                                                                                                                                                                                                                                                                                                             ----GYGGLGSQGAGRG---
                                                                                                                                                                                                                                           -GLGNQGAGRGGLG
                                                                                                                         -GLGSQGSGRGGLG-----
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-gqgagaaaaaaggagqgg

136

300 183

240

420

360

284

-----GQGAGAAA

-GQGAGAAAAAAAGG

545

494 599 439 540 398 480

648 775 589

major ampullate fibroin protein - orb spider (Nephila clavip C;Species: Nephila clavipes C;Date: 08-Mar-1991 #sequence_revision 13-Jan-1993 #text_cha C;Accession: A36068 R;Ku, M.; Lewis, R.V. Proc. Natl. Acad. Sci. U.S.A. 87, 7120-7124, 1990 A;Title: Structure of a protein superfiber: spider dragline A;Reference number: A36068; MUID:90384959; PMID:2402494 A;Accession: A36068 -references: UNIPROT:P19837; GB:M37137; NID:g159711; PID:g159712 the authors translated the codon GGT for residue 292 as Gln, GTA Score 1041; DB 2; Pred. No. 1.6e-55; Mismatches 305; (Nephila clavipes) #text_change 09-Jul-2004 Length 718; Indels 138; silk. (fragment) Gaps for 60

61 GAGAGSGAGAGSGVGVPGVGVPGVGVPGKGVPGVGPGVGPGVGPGVGPGAGAGSGAGAGS 1 GAGAGSGAGAGSGVGVPGVGVPGVGVPGVGVPGVGPGVGPGVGPGAGAGSGAGAGS GAGAGSGAGAGSGVGVPGVGVPGVGVPGKGVPGVGPGVGPGVGPGVGPGAGAGSGAGAGS AAAAG---GAGQG-----GYGGLGSQGAGRG---------GQGAGAAA 120 180 78 47 residue

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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Rccession: A70869

A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-1660 <COL>
A;Cross-references: UNIPROT:053215; GB:AL021246; GB:AL123456; NID:g3261507; PIDN: A;Experimental source: strain H37Rv
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C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical glycine-rich protein Rv2490c - Mycobacterium tuberculosis (strain C;Species: Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004 C;Accession: A70869
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Best Local Similarity
Matches 340; Conserv
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                                                                                                                                                                                                                          EDGGNGGAGGAGGAHAGDGGAGGAGGNGGAGGNGAHGFNAVLVSDGGNGGDG--
                                                                                                                                                                                                                                                              GGNGAHAPVAGGHGGNGGAGGNGGLVGDGGAG
                                                                                                                                                                                                                                                                                                                                                                              NGGSWLAAGDGGAGGHGGDPGLG-GAGGAGGASGGAGARAGANGLAAGNDGPVSGGNGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGAGSGAGAG----SGAGAGSGYGVPGV-----GVPGV-----GVPGKGVPGV--G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGAGSGAGAGSGVG-----VPGVGVPGVGVPGKGVPGVGPGVGPGVGPGVGPGAGAGS
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                                   --GAG-----SGAGAGSGVGVPGVGVPGVGVPG----KGVPGVGP---
                                                                                                            GKGVPGVGPGVGPGVGPGAGA-------GSGAGAGSGA------
                                                                                                                                                                                     PGVGPGVGPGVGPGAGAGSGAGAGSGAGAGSGAGAGSGVGVPGVPG------VGVP
                                                                                                                                                                                                                                                                                                                                         AGSGA-----GAGSGVGVPGVGVPGVGVPGKGVPGVG-----
                                                                                                                                                                                                                                                                                                                                                                                                                 PG-----VGVPGKGVPGVGPGVGPGVGPGVGPGAGAGSGAGA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGGAGGVGGNGGRGGWLLGNGGAGGVGGVGGAGGAGGAGGAG-GAGATGINGPAGISAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGVGPGVGPGVGPG-----AGAGSGAGAGSGAGAGSGAGAGSGVGVPGVGVP-GVGVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAG-GAGGNAGWFGHGGAGGVGGVGAAGANGATPGQDGAAGVAGSDDGAGGDGLAGSDGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGGAGGAGAPGGTGGWLAGGGGVGGMGGAGGAGGAGGNAGLFGNGGAGGAGGAGG
KGGAGGNGGLVGDGGAGGDGGSGAAGANGANVGEDGADGTLSGQPGEGSEANGGQGGVGG
                                                                        GAGGDGGDPGAG----GKGGAGGAGATEGVTGATGATVHSGGNGGKGGNGADATVAGANGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GDGGAGGNGGAGGNGGVGGAGGAGGSAGLLGYVGRAGDG-GAGGGGGLGGAPGDGGAGG
                                                                                                                                                 - GAGGRGGDGGAGGAGGDAPAGRAGSQGVGGDGGAGGAGGAPGNGGSGGRGDMAFKDGDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 1034; DB 2; ; Pred. No. 7.9e-55; 22; Mismatches 395;
                                                                                                                                                                                                                                                                                                     -GHGGDGAAGAGYADMTAIFLGSSGTPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1660;
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                                     GVGP
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N.; Holroyd,
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A;Authbors: Sqares, R.; Suleton, J.E.; Taylor, K., Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70917
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C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: strain C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             24.2%; Score 1010.5; DB 2; 33.8%; Pred. No. 1.7e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H37Rv
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                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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676 VPGVGVPGVGVPGK-----GVPGVGPGVG-PGVGPGVGPGAGAG-------SGAGAGS
                                                                                                                                                                                                                                                              929 TRAASGVDASDHGPGSGGNGGNGGNGAQASVAGGAGGNGGDGGNAGRVGDGGAGGNGGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        814 GAGGAGASGGGGKGASGADSAEAVGGAGGKGGDGGVGGVG--GDGGPGGDGGAGGAAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVGPGVGPGAGAGSGA-GAGSGAGAGSGAGAGSGVGVPGVGVPGVGVPGKGVPGVGPGVG
                                                         GAGAGSGAGAGSGVGVPGV-GVPGVGVPGVGVGVGPGVGPGVGPGVGPGAGAGSGAGA
GAGGNGGVGASGGAGARGANGIDSIG----GTGGAGGGGGGGGAGGVGGHGGDGGVGGA
                                                                                                                             AAGANGANSGAPGSDALALGQPGGNGGQGDAGQAGGAGGAGGAGGAGGSVSGDGGAGGNG
                                                                                                                                                                                                                                                                                                                                                                                              GQVGSHGVG-GVGGDGGLGGAGGNGGDGGDGGDGGDFGAG--GLGGLGGDSGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAGGAGGDGGAGSSALGSGGNGGRGDAGQAGGAGGAGGAGGAGGSVSGDGGPGGKGGAG
                                                                                                                                                                                                                                                                                                                              -KGVPGV-----GPGVGPGVGPG-----VGPGAGAGSGAGAGSGAGAGSGAGAGSGVG
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Mycobacterium tuberculosis (strain H37RV)

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: E70917

collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology Length 1329;

1 GAGAGSGAGAGSG--VGVPGVGVPG------VGVPGKGVPGVGPGVGP G---GVGGTGGAGGLGGTLYGAGGHGGAGGPGPIGGVGGHGGVGGAAGLLGVGGHG-GAG GVGPGVGPGAGAGS-----GAGAGSGA-----GAGSGAGAGSGVGVPGVGVPGVGVP GAGAAGGAGGSGGWLLGNGGVGGAGGQSLLGGATGGAGGNAGLFGVGGTGGPG-GPG GAGAGSGAGAGSGVGVPGVGVPGVGVPGVGPGV-GPGVGPGVGPGAGAGSGAGAG GGKAGGNGGAGGAGGLVGNGGAG-GAGGNGAPGAPPSGGDPNGGGGGAGGAGGKGGDGGA GAGAGSGAGAGSGVGVPGVGVPGVGVPGKGVPGVGPGVGPGVGPGVGPGAGAGSGAGAGS VG-----VPG--VGVPGVGVPGKGVPGVGPGVGPGVGPGAGAGAGA-----GS GKGVPGVGPGVGPGVGP-----GVGPGAGAG------SGAGAGSGAGAGSGAGAGSG 133 AGFSRALIVAGDNGGDPGAGGAG-GTGGAGSTIGAHGAAGASPTSGGNGGAGGNGAHFSS GHGAEGVAGAAGEDLSPHGTSGGVGGDAGDGGTGGRGGWLAGAGGAGGAGGVGGTGGAGG Indels 249; Gaps 468 409 180 87 240 350 290 234 40 47

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RESULT 14
E70806
E70806
hypothetical glycine-rich protein Rv3507 - Mycobacterium tuberculosis (strain C;species: Mycobacterium tuberculosis
C;pecies: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: E70806
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.
R;Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S
Nature 393, 537-544, 1998
A;Authors: Squres, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the compl
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70806
                                                                                   A; Experimental C; Genetics:
                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not
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                                            ;Gene: Rv3507
;Superfamily:
             Query
 Best
 Local Similarity
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Score 1006;
Pred. No. 3
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DB 2;
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RESULT 15
A70934
Aypothetical glycine-rich protein Rv0578c - Mycobacterium - hypothetical glycine-rich protein Rv0578c - Mycobacterium - hypothetical glycine-rich protein Rv0578c - Mycobacterium - hypothetical glycine-rich protein C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: A70934
C;Accession: R70934
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
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727	VGFGVGFGVGFGAGAGGSGAGAGSGV-GVPGVGVPGV	Db 668
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492	GVPGVGVPGKGVPGVGPGVGPGVGPGAGAGSGAGAGSGAGAGSGAGAGGAGAGAGAGAGAGAG	Qy 200 Db 435
434	GAGGAGGASVGGSAHGANGAPGTTSTSGGNGGDGKGADAISSGQTGANGGRGGDGG	Db 375
199	GVGPGVGPGVGPGAGAGAGAGAGAGSGAGAGAGAGAGAGAGSGVGVPGV	Оу 157
374	GVGPGVGPGVGPGAGAGAGAGAGAGAGAGAGAGAGAGAGA	Qy 97 Db 316
315	GAGGAGGVLMGNGGNGGAGGEGGPGGAGGAGGAGAGSGAHATNLGADGQAGGNGGNGGAGGTGG	Db 256
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	9c : collagen alpha 1(IV) chain	A;Gene: Rv0578c C;Superfamily:
; PIDN:CAA174	COL> UNIPROT:053775; GB:AL021942; GB:AL123456; NID:g3242298 e: strain H37Rv	A;Residues: 1-1306 < A;Cross-references: A;Experimental sourc
shown	y; nucleic acid sequence not shown; translation not	Status:
1, B.G. complete genome	: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, Deciphering the biology of Mycobacterium tuberculosis from the cocce number: A70500; MUID:98295987; PMID:9634230	;Authors; ;Title: ;Referen

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1130 GTGGTGGAGGAGGTGS 1145	765 GVGPGAGAGSGAGAGS 780	1075 SPTGNNGSQGAGGDGGAGGTGGTGGTGGDGGRGAHGTLFSSLAGTGGTGGNGGTG- 1129	GAGSGAGAGSGVGVPGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVG	1015 GGAGGTGGTGLRGTTGATGATGTFDAGADGHGGNGGTGGVGGTGGAGGGGGNGGAGGKAL 1074	696 PGVGPGVGPGV 722

Search completed: December 30, 2004, 12:59:00 Job time: 51 secs

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Aat08433 kukulcania
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O95iu8 argiope tri
O17434 nephila cla
O6fpro candida gla
O95pro candida gla
O99hw2 nephila ina
P07916 drosophila
O99bit7 plectreurys
O99hw4 nephila cla
O99bit7 plectreurys
O99hw4 nephila cla
O99bit7 drosophila
O94359 nephila cla
O806918 mus musculu
O94350 mus musculu
O99372 rattus norv
O77u48 drosophila
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ALIGNMENTS

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PARTIAL SEQUENCE FROM N.A. MEDLINE=93565842; PubMed=7916056; Mita K., Ichimura S., James T.C.; "Highly repetitive structure and its organization of the silk fibroin gene."; J. Mol. Evol. 38:583-592(1994). [6] SEQUENCE OF 5179-5263 FROM N.A., AND DISULFIDE BONDS. STRAIN=J-139;	PARTIAL SEQUENCE FROM N.A. STRAIN=Kinshu X Showa; MEDLINE=89094868; PubMed=3210244; Mita K., Ichimura S., Zama M., James T.C.; "Specific codon usage pattern and its implications on the secondary structure of silk fibroin mRNA."; J. Mol. Biol. 203:917-925(1988).	CeIl 18:591-600(1979). [3] PARTIAL SEQUENCE FROM N.A. MEDLINE=79211211; PubMed=455439; Tsujimoto Y., Suzuki Y.; "Structural analysis of the fibroin gene at the 5' end and its surrounding regions."; Cell 16:425-436(1979).	SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=20330362; PubMed=10871375; Zhou CZ., Confalonieri F., Medina N., Zivanovic Y., Esnault C., Zhou CZ., Confalonieri F., Medina N., Zivanovic Y., Esnault C., Yang T., Jacquet M., Janin J., Duguet M., Perasso R., Li ZG.; "Fine organization of Bombyx mori fibroin heavy chain gene."; Nucleic Acids Res. 28:2413-2419(2000). SEQUENCE OF 1-168 FROM N.A. SEQUENCE OF 1-168 FROM N.A. MEDLINE=80045039; PubMed=498286; TSUJimoto Y., Suzuki Y.; TS	1 5

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EMBL; V00094; CAA23432.1; -.
EMBL; V00097; CAA23433.1; -.
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EMBL; X13869; CAA32776.1; -.
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"Determination of the site of disulfide linkage between heavy and light chains of silk fibroin produced by Bombyx mori.";

Biochim. Biophys. Acta 1432:92-103(1999).

-i- FUNCTION: Forms the silk filament; a strong, inextensible, insoluble and chemically inert fibre.

-i- SUBUNIT: Formed of two chains: heavy and light, that are linked by a disulfide bond. Heavy-light chain assembly is essential for the efficient intracellular transport and secretion of fibroin.

-i- TISSUE SPECIFICITY: Produced exclusively in the posterior (PSG)
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DISULFID
CONFLICT
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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BL; X13869; CAA32076.1; -.
BL; M35378; AAA27839.1; -.
BL; AB017362; BAA33147.1; -.
R; S01844; S01844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            section of silk glands.

DOMAIN: Composed of antiparallel beta sheets. The strands of the beta sheets run parallel to the fiber axis. Long stretches of silk fibroin are composed of microcrystalline arrays of (-Gly-Ser-Gly-Ala-Gly-Ala-)n interrupted by regions containing bulkier residues.
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Pred. No. 3.3e-99;
5; Mismatches 234;
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Fibroin heavy characteristics
HIGHLY REPETITIVE
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Q6Q294;
Q6Q294;
Q5-JUL-2004 (TrEMBLrel. 27, Created)
Q5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Q5-JUL-2004 (TrEMBLrel. 27, Last amountation update)
M5-JUL-2004 (TrEMBLrel. 27, Last amountation update)
Major ampullate spidroin (Fragment).
Agelenopsis aperta (Funnel-web spider).
Bukaryota; Metazoa, Arthropoda; Chelicerata; Arachnida;
Araneomorphae; Entelegynae; Agelenidae; Agelenopsis.
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                                             AAT08436 PRELIMINARY; PRT; 897 AA.

AAT08436;
12-MAY-2004 (TrEMBLrel. 27, Created)
12-MAY-2004 (TrEMBLrel. 27, Last sequence update)
12-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Major ampullate spidroin (Fragment).
Agelenopsis aperta (Funnel-web spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;
Araneomorphae; Entelegynae; Agelenidae; Agelenopsis.
NCBI_TaxID=6908;
SEQUENCE FROM N.A.
Tian M., Liu C., Lewis R.;
"Analysis of Major Ampullate Silk
Spiders.";
Biomacromolecules 0:0-0(2004).
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Best Local Similarity
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NON TER 1 1
SEQUENCE 897 AA; 70174 M
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50.8%; Pred. No. 5e-90;
ive 66; Mismatches 2
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STIRLING OCCUPA

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735

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Query Match
Best Local S
Matches 401
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Major ampullate spidroin 1 (Fragment).
Kukulcania hibernalis (Southern house spider).
Kukulcania hibernalis (Southern house spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Haplogynae; Filistatidae; Kukulcania.
NCBI_TaxID=268415;
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EMBL; AY571308; AAT08433.1; -.
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760 AA;
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Pred. No. 1.4e-70;
7; Mismatches 224;
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AAT08433;
12-MAY-2004 (TrEMBLrel. 27, Created)
12-MAY-2004 (TrEMBLrel. 27, Last sequence update)
12-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Major ampullate spidroin 1 (Fragment).
Kukulcania hibernalis (Southern house spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;
Araneomorphae; Haplogynae; Filistatidae; Kukulcania.
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Tian M., Liu C., Lewis R.;
"Analysis of Major Ampullate Silk cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spiders.";
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46.3%; Pred. No. 1.4e-70;
vative 37; Mismatches 224
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                                                                                                                                                                                                                MEDLINE=21179804; PubMed=11283372; Gatesy J., Hayashi C., Motriuk D., "Extreme diversity, conservation, & fibroin sequences.";
                                                                                                                                                                                                                                                          Argiope trifasciata (Banded garden spider).
Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Araneoidea; Araneidae; Argiope.
NCBI_TaxID=156845;
                                                                                                                                                                                                                                                                                           Name=Flag;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence up
01-JUN-2003 (TrEMBLrel. 24, Last annotation
Flagelliform silk protein (Fragment).
                                                                                                                                                                                   Gateву J
                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                        fibroin sequences.";
Science 291:2603-2605(2001)
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                              interPro;
                                                                                                                                          esy J.E., Hayashi C.Y.;
mitted (FEB-2001) to the EMBL/GenBank/DDBJ
L; AF350265; AAK30594.1; -.
GO:0005737; C:cytoplasm; IEA.
GO:0006817; P:phosphate transport; IEA.
errbro; IPR008160; Collagen.
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AGGFGPGGAGGYGPG-GVGPGGAGGFGPG-GVGPGGSGPGGAGGEGPVTVDVDVSVGGAP
                                                            GAGPGGAGGEGPVTVDVDVTVGPEGVG-GGPGGAGPGGAGFGPGGAGFGPGGAPGAPGG
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Minor ampullate silk protein MiSpl (Fragment).
Nephila clavipes (Orb spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;
Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae;
NCBI TaxID=6915;
EMBL; AF027735; AAC14589.1;
NON TER 1 1
SEQUENCE 988 AA; 79082 MY
                                                               Colgin M.A., Lewis R.V.;
"Spider minor ampullates silk proteins and highly conserved non-silk-like 'spectain Sci. 7:667-672(1998).
                                                                                                                                                         MEDLINE=98200471; PubMed=9541398;
                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                        AGAAAAAGAGAG-GAGYGRGAGAGAGAAAGAGAGAAAGA-GAGAGGYG--GQGGYGAGAG
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                                                                                             GGYG-RGAGAGGYGGQG-
                                                                                                                            PGVGVPGVGVPGVGPGVGPGVGPGVGPGAGAGSGAGAG
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39.4%; Pred.
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Pred. No. 1.8e-66;
6; Mismatches 286
                   PRT;
                                                                                               -GYGAGAGAGAAAAAGAGAG
                   1553
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A Lafontaine I. de Montigny J., Marck C., Neuveglise C., Talla E.,
A Lafontaine I. de Montigny J., Marck C., Neuveglise C., Talla E.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.
A Boffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet F., Kachouri R.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet F., Kachouri R.,
A Kerrest A., Kogzul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Kerrest A., Kogzul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropulos O.,
A Pellenz S., Potter S., Richard G.F., Straub M.L., Suleau A.,
A Penlenz S., Potter S., Richard G.F., Straub M.L., Suleau A.,
A Seminum P., Takaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
A Seminum P., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
A Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.
Wincher P., Souciet J.L.;
B. Wincher P., Souciet J.L.
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORFNames=CAGL0J01771g;
Candida glabrata (Yeast) (Torulopsis glabrata).
Cuandida glabrata (Yeast) (Torulopsis glabrata).
Eukaryota, Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Similarities with tr|Q08294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 430:35-44(2004)
EMBL; CR380956; CAG607
SEQUENCE 1553 AA; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENOLEVURES
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VCE 1553 AA; 145623 MW;
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                                                                                                                                                                                                                                                                                                        APGEGSGSGSGSG-
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    AGAGSGAGAGSGAGAGSGVGVPGVGVPGVGVPGKGVPGVGPGVGPGVGPGVGPGAGAGSG
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Last annotation update)
Saccharomyces cerevisiae
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Best Local Sim
Matches 412;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation updat
Flagelliform silk protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=20156786; PubMed=10688794;
Hayashi C.Y., Lewis R.V.;
"Molecular architecture and evolut:
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                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nephila inaurata madagascariensis.
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;
Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Flag;
                                                                                                                                                                                                                                                                                                                                                        Science
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                                                                                                                                                                                                                                                                                                     ence 287:1477-1479(2000).

IJ, AF218623; AAF36091.1; -..

IGO:0005737; C:cytoplasm; IEA.

GO:0006817; P:phosphate transport;

GPPTO; IPR008160; Collagen.
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            GSGVGVPGVG---
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                                                                                                           GPG----AGAGSG-----AGAGSGAGAGSGAGAGSGVGVPGVGVPGVGVPGKGVPG
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Pred. No. 6.2e-
16; Mismatches
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P07916;

01-AUG-1988 (Rel. 08, Created)

1 01-AUG-1988 (Rel. 08, Last sequence up

1 05-UUL-2004 (Rel. 44, Last annotation

1 07-AUG-1988 (Rel. 47, Last annotation)
SEQUENCE FROM N.A.

MEDLINE-87243230; PubMed=3593675;

Bressan G.M., Argos P., Stanley K.K

"Repeating structure of chick tropo
DNA cloning.";

Biochemistry 26:1497-1503(1987).

[2]
                                                                                                                                Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                             NCBI_TaxID=9031;
                                                                                                                      Archosauria;
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                                                                                                                      Aves;
                                                                                                                      Neognathae;
                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                   Stanley K.K.; chick tropoelastin
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EMBL; M18633; AAA48761.1; -.
EMBL; M2180; AAA49082.1; -.
EMBL; M1580; AAA49108.1; -.
EMBL; M15809; AAA49108.1; -.
PIR; A26601; A26601.
InterPro; IPR008160; Collagen.
InterPro; IPR003979; tropoelastin.
Pfam; PF01391; Collagen; 1.
PRINTS; PR01500; TROPOELASTIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 85-750 FROM N.A. (ISOFORM MEDLINE=88309083; PubMed=2841924; Baule V.J., Foster J.A.; multiple chick tropoelastin mRNAs.";
                                                                                                                                                                                                                                                                                                                       Structural
                                                                                                                                                                                                                                                                                                                                PRINTS; PR01500; TROPOELASTIN.
Alternative splicing; Connective tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <del>-</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h. Biochem. Biophys. 256:455-461(1987).
FUNCTION: Major structural protein of tissues nuchal ligament, which must expand rapidly and SUBUNIT: The polymeric elastin chains are crost into an extensible 3D network.
SUBCELLULAR LOCATION: Extracellular matrix of ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: The crosslinks are made
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=2; Synonyms=Embryonic;
IsoId=P07916-2; Sequence=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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Allysine (Potential).
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RA Adams N.D., Celnikers S.E., Holt R.A., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton R.C., Rogers Y.H., Blazej R.G., Champe M., Pfesiffer B.D.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfesiffer B.D.,
RA Ballew R.M., Basu A., Baxer B.G., Helt G., Nelson C.R., Gabor G.L.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Borttier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.N.,
RA docison K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA dolden R., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Fosler C., Gabrielian A.B., Gary N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Alakin D., Houston K.A., Howland T.J., Wei M.H., Tbeysann C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lianko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Mozris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Mozris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Suuskern D.R., Pacleb J.M.,
RA Rainert K., Remington K.A., Saunders R.D., Scheeler F., Shen H.,
RA Mang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Mang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Sheng X.H., Zhong F.N., Zhong G., Zhao Q., Zheng L.,
RA Schence 287:2185-2195(2000).
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Berman B.P.
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Kaminker J.S., Bergman C.M., Kronmiller
Patel S., Frise E., Wheeler D.A., Lewis
Ashburner M., Celniker S.E.;
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GSGVGVPGVGV-PGVGV-PGKGVPGVG--PGVGPGVG---PGVG--PGAGAGSGAGAGSG
                                                      GAQPGVGAQTGAGQPGYGSQPGIGGQTGAG-QPGYGSQPGIGGQTGARQPGYGSQPGVGA
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MEDLINE=21179804; PubMed=11283372;
Gatesy J., Hayyashi C., Motriuk D., Woods J., Lewis
"Extreme diversity, conservation, and convergence
"Extreme diversity,";
                                                                                               Q9BIT2 PRELIMINARY; PRT; 912 AA.
Q9BIT2;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Fibroin 1 (Fragment).
Plectreurys tristis (Spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;
Araneomorphae; Haplogynae; Plectreuridae; Plectreurys.
NCBI TaxID=33319;
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Best Local S
Matches 334
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF350281; AAX30610.1; -.

NON TER 1

SEQÜENCE 912 AA; 74131 MW; 0A9FE14AA60D3EB5 CRC64;
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                                                            GVGPGAGAGSGAGA-GSGAGAGSGAGAGSGVGVPGVPG----
                                                                                           AAAAAAAAAAAGAGAGAGAGAGAGAGAGSGAST----SVSTSSSSASGAGAGAGSGAGS
                                                                                                                                       GAGGAGAGFGSGLGLGYGVGLSSAQAQAQSAAAARAQADAQAQAQAQAQAQAQAQAQAQAQAQ
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                      ---- AGAGSGAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGVPGKGVPGVGPGVGPGVGP
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Best Local Similarity
Matches 418; Conserv
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Flagelliform silk protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON TER
NON TER
SEQUENCE
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Nephila clavipes (Orb spider).

Rephila clavipes (Orb spider).

Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;

Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae; Nephila.

NCBI_TaxID-6915;
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Hayashi C.Y., Lewis R.V.;
"Molecular architecture and evolut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9NHW4
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GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0006817; P:phosphate transport; IEA.
InterPro; IPR008160; Collagen.
InterPro; IPR000209; Pept S8 S53.
PROSITE; PS00138; SUBTILASE_SER; UNKNOWN_1.
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 P-GVGP-----GVGPGAG--AGSGAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGVPGKG
                                                                                                                                                                        GP-GVGPGAGAGSGAGAGS----GAGAGSGAGAG----SGVGVPGVGVPGVGVPGKGVP-
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                             AGGPYGPGGAGGPYGPGGAGGSYGLGGAGGSGGVGPGGSGPGGYGPGGAGPGGYGPGGSG
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Pred. No. 1e-58;
8; Mismatches 3
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                            Query Match
Best Local Similarity
Matches 397; Conserv
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Q9BIT7;
01-JUN-2001
01-JUN-2001
                                                                                  NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sanotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Major ampullate spidroin 2-like protein (Fragment).
Mephila inaurata madagascariensis.
Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida,
Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae;
                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINB=21179804; PubMed=11283372;

Gatesy J., Hayashi C., Motriuk D.,

"Extreme diversity, conservation, a
fibroin sequences.";
                                                                                                                                         Gatesy J.E., Hayashi C.Y.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ
                                                                                                                             EMBL; AF350276; AAK30605.1;
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                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                   Science 291:2603-2605(2001).
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 GAGAGSGAGAGSGVGVPGVGVPGVGVPGKGVPGVGPGVGPGVGPG-VGPGAGAGSGAGAG
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1953
                          31.1%; Score 1297.5; DB 2; ilarity 36.4%; Pred. No. 1.7e-58; Conservative 32; Mismatches 324;
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AA; 1
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Best Local (
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Development 129:3741-3253(2002).
EMBL; AF203342; AAF13280.1; -.
FlyBase; FBgn0028573; prc.
GO; GO:0005578; C:extracellular matrix; IDA
GO; GO:0007507; P:heart development; IMP.
'InterPro; IPR009765; Pericardin rpt.
Pfam; PF07054; Pericardin rpt; 33.
SEQUENCE 1729 AA; 164661 MW; DA9B1B7FAE
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Q9U617;
01-MAY-2000
01-MAY-2000
01-MAR-2004
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Name=prc;

Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo.

Bendoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

MCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22065272; PubMed=12070098; Chartier A., Zaffran S., Astter M., Semeriva M., Gratecos D.; Chartier A., Zaffran S., Astter M., Semeriva M., Gratecos D.; "Pericardin, a Drosophila type IV collagen-like protein is involved the morphogenesis and maintenance of the heart epithelium during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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QPGIGGQTGAAQPGYGTQPGVGAQTGTGQPGYGAQPGIGGQTGAGQPGYGRQPGIGGQTG
                            GSGAGAGSGVGVPGVGV-PGVGV-PGVGV-PGVGP--PGAGAGSG
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Search completed: December 30, 2004, 12:54:58	GYGFGSQFGIGGAPVYGTQPGGGGQTGVIGG 1207	בווים ביווים		GAGSGAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGVPGKG-VPGVG 756	YGNQPGVGGQTGAGQPGYGSQPGVGGQTGAGQPGYGVIPGFGGQPGIGGQTAAGKPGY 1116	AGAGSGAGAGSGVGVPGVG-VPGV-GVPGKGVPGVGPGVGPGVGPGVGPGA 710	QPGIGGQTGAGQPGYGSQTGVGGQIGAGQPGYGAQPGYGAQPGYGAQPGFGGQPG 1058	VPGV-GVPGKGVPGVGPGVGPGVGPGAGAGSGAGAGSG 661	PGFGGQPGIGGQTGAGQPGYGFIGQPGIGGQTGTSGRQPGYGTQPGIGGQTAAGQPGYGS 998	PGVGPGVGPGAGAGSG-AGAGSGAGAGSGAGAGSGVGVBGVG- 620	QPGISGQTGGGQPGYGGQATISGLPGYGTQPGIGALTAVPGGGHYGYETQPGIGGQTGTNQ 938	GSGV	LTQPGIGGISGPIGGKVGGGQSEAAKPGYWAQPGIGGPSRYGSQPGIGDQTGAGQSGYGG 878	PGVGPGVGPGAGAGSGAGAGSGAGAG-SGAGA 550	QIGGQTGAGQPS-YGSQPGVGAQNGGGQPGYGTRPVIGGQTGAGQPGYGGQTGVGGSPGF 818	GAGAGSGAGAGSGAGAGSGVGVPGVGVPGV 519	PGQ-PGYGTQPGVGTQTGTGQPGYGAQPGIGGQSGAGQPGYGSQPGIGGQTGGGDTGGGPGYGS 759	AGAGSGAGAGSGAGAGSGVGVPGVGVPGV-GVPGKGVPGVGPGVGPGVGPGVGP 468

Search completed: December 30, 2004, 12:54:58 Job time : 215 secs

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Result
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Perfect score:
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-08-175-155-47
US-08-175-155-47
US-08-175-155-82
US-08-175-158-82
US-08-18-97-633A-54
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US-08-806-029-27
PCT-US95-02772-4
US-08-806-029-35
US-08-175-155-39
US-08-175-155-39
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ALIGNMENTS

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; TOPOLOGY: unknown ; MOLECULE TYPE: protein US-08-806-029-19
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Query Match
Best Local Similarity
Matches 765; Conserv
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                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/806,029
FILING DATE: 24-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION MOMBER: US 08/212,237
FILING DATE: 11-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: 3-58847-2/;
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                      TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cappello, UDBERT.

APPLICANT: Stedronsky, Erwin R.

TITLE OF INVENTION: Synthetic Proteins for in vivo Drug
TITLE OF INVENTION: Delivery and Tissue Augmentation
NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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CITY: San Francisco
STATE: California
COUNTRY: United State
                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: unl
                                                                                                                                                                                                 LENGTH: 889 amino acids
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    Conservative
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                    84.5%;
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Score 3526; DB 3;
Pred. No. 3.3e-252;
0; Mismatches 13;
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                                           Length 889;
    Indels 52;
  Gaps
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RESULT 2
US-08-397-633A-68
                                                                                                                       Sequence 68, Application Patent No. 5773577 GENERAL INFORMATION:
                                                                 APPLICANT: Cappello, Joseph
TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
        ADDRESSEE: FLEHR, HOE
STREET: 4 Embarcadero
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
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INFORMATION FOR SEQ ID NO: 68
SEQUENCE CHARACTERISTICS:
LENGTH: 884 amino acids
TYPE: amino acid
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Matches
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Best Local
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/397,633A
FILLING DATE;
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-58848-1/
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
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Pred. No. 1.8e-246;
0; Mismatches 26;
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US-08-435-641-15
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                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I.
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-61127
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Stedronsky, Erwin R.
APPLICANT: Stedronsky, Erwin R.
TITLE OF INVENTION: Tissue Adhesive Using Synthetic
TITLE OF INVENTION: Crosslinking
                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 884 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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CITY: San Francisco
STATE: CA
COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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Pred. No. 1.8e-246;
0; Mismatches 26;
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US-08-707-237A-96
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Patent No. 58
       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0; Vers
SOFTWARE: PatentIN DATA:
APPLICATION NUMBER: US/08/707,237A
FILING DATE: 03-SEP-1996
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
OR OF CLASSIFICATION DATA:
OR OF CLASSIFICATION NUMBER: US/08/175,155
                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                  APPLICANT: Ferrari, Franco A.
APPLICANT: Capello, Joseph
APPLICANT: Crissman, John W.
APPLICANT: Dorman, MATY A.
TITLE OF INVENTION: METHODS FOR PREPARING SYNTHETIC
TITLE OF INVENTION: REPETITIVE DNA
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test,
STREET: Four Embarcadero Center,
                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                           STATE: California
COUNTRY: United States
ZIP: 94111-4187
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CITY: San Francisco
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JMBER: US 08/175,155
29-DEC-1993
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Suite 3400
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; TOPOLOGY: ur ; MOLECULE TYPE: US-08-707-237A-96
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Best Local :
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INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 884 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 06/927,258 FILING DATE: 04-NOV-1986 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 0 FILING DATE: 29-OCT-1987 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 1
FILING DATE: 06-NOV-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-10/WHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 09-NOV-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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Similarity 90.6%;
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                 GVG-PGVG-PGAGAGSGAGAGSGAGAGSGVGVPGVGVPGVGVPGKGVPGVG-PG 397
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Pred. No. 1.8e-246;
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RESULT 5
US-08-642-246-15
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US-08-642-246-15
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GENERAL INFORMATION:
                                                                                                                     Matches
                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: STEDRONSKY, Erwin R.
APPLICANT: CAPPELLO, Joseph
TITLE OF INVENTION: Crosslinking
TITLE OF INVENTION: Crosslinking
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLIER, HOHBACH, TEST, ALE
STREET: FOUR Embarcadero Center, Sui
                                                                                                                                                                                                                                                                                    TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A611
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                       STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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: CA
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                                                                                                                  Score 3448; DI
Pred. No. 1.8e:
0; Mismatches
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US-09-451-206-15
; Sequence 15, Application US/09451206
; Patent No. 6423333
; GENERAL INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST,
STREET: Four Embarcadero Center,
                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                      TITLE OF INVENTION: Tissue Adhesive Crosslinking
                                                                                                                                                  APPLICANT:
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CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
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Best Local :
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REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A61127-1/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/642, FILING DATE: <Unknown> ATTORNBY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/451,206
FILING DATE: 29-No. 642333-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
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90.6%;
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Pred. No. 1.8e-246;
0; Mismatches 26;
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RESULT 7
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: STEDRONSKY, Erwin R.
APPLICANT: CAPPELLO, Joseph
TITLE OF INVENTION: Tissue Adhesive Using Synthetic
TITLE OF INVENTION: Crosslinking
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Best Local Similarity
Matches 752; Conserv
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SEQUENCE CHARACTERISTICS:
LENGTH: 884 amino acid
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A611
TELECOMMUNICATION INFORMATION:
TELECPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06229
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PR: A61127-1/BIR
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Pred. No. 1.8e-246;
0; Mismatches 26;
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Suite 200
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GENERAL INFORMATION:
APPLICATION NUMBER: US/08/175,155
FILING DATE: 29-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROwland, Bertram I.
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-55186-5/
TELECOMMUNICATION INFORMATION:
                                                                                                              ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, V
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ferrari, Franco A. APPLICANT: Cappello, Joseph APPLICANT: Crissman, John W. APPLICANT: Dorman, Mary A.
                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                     APPLICANT: Dorman, Mary A.
TITLE OF INVENTION: Methods for Preparing Synthetic
TITLE OF INVENTION: Repetitive DNA
NUMBER OF SEQUENCES: 69
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STATE:
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                 A-55186-5/BIR
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; INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2257 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-175-155-47
                                                                                                                                                                                                                                                                                                             Query Match 79.0%;
Best Local Similarity 67.4%;
Matches 755; Conservative
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5.8e-235;
nes 25;
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Pred. No. 5.8e-235;
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Pred. No. 5.8e-235;
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  Query Match
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Matches 755
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
PRIOR APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
APPLICATION NUMBER: US 08/175,155
FILING DATE: 22-APR-1993
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F:
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: 31-55186-6/RE
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                       TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                    TOPOLOGY: 1: MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION UNMERS. UF (201/40)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Richardson, Charles
APPLICANT: Chambers, James
APPLICANT: Causey, Stuart
APPLICANT: Causey, Stuart
APPLICANT: Causey, Stuart
APPLICANT: Crissman, John W.
APPLICANT: Crissman, John W.
TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
NUMBER OF SEQUENCES: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400
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CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94111
  Local Similarity hes 755; Conserv
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STRANDEDNESS: sil
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Score 3296; DB 3;
Pred. No. 5.8e-235;
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                                               Length 2257;
    Indels 340;
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                                                                                                                                                                                                                                                                                                  ; STRANDEDNESS: single; TOPOLOGY: linear; MOLECULE TYPE: peptide; SEQUENCE DESCRIPTION: 
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US-09-444-791A-82
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Patent No. 6355776
GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A.
                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 2257 amino ac:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/482,085
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
                                                                                                                                                                                                     Local Similarity
les 755; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PETENTIA Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSE: Flehr Hohbach Test Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
98
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                                                                                                                             APPLICATION NUMBER: US/09/444,791A FILING DATE: 22-No. 6355776-1999 CLASSIFICATION: <Unknown>
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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Crissman, John W.
OF INVENTION: No. 6355776el Peptides Comprising Repetitive
Units of Amino Acids and DNA Sequences Encoding the
                                                                                                                                                                                                     79.0%; ilarity 67.4%; Conservative
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Pollock, Thomas J.
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                               SEQ ID
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                                                                                                                                                                                                  Score 3296; DB 3;
Pred. No. 5.8e-235;
0; Mismatches 25;
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RESULT 13
US-08-397-633A-54
; Sequence 54, Application
; Patent No. 5773577
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Best Local (
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,633A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: DOLLAGE BOTTOM:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 877 amino
TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cappello, Joseph
TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: C
                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco
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California
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Pred. No. 2e-234;
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ATTORNEY/AGENT INFORMATION:

NAME: ROWLAND, BETTRAT

REGISTRATION NUMBER: 20,015

REFERENCE/DOCKET NUMBER: A-58!

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-781-1989

TELEPHONE: 415-781-1989

TELEPHONE: 415-781-1989

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE TYPE: B32 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: brotein

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US-08-212-237-4
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                                                   Query Match 78.0
Best Local Similarity 88.0
Matches 742; Conservative
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/212,237
FILING DATE: 11-MAR-1994
CLASSIFICATION: 435
CCLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: Cappel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Synthetic Prote
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test,
STREET: Four Embarcadero Center,
                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A. ZIP: 94111-4187
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STATE: CA
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Synthetic Proteins As
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                                                   Score 3253; DB 1;
Pred. No. 3.6e-232;
0; Mismatches 13;
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Suite 3400
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                                             US-08-805----

Sequence 27, Applicac...

Patent No. 6380154

PAPLICANT: Cappello, Joseph
APPLICANT: Stedronsky, Erwin R.

TITLE OF INVENTION: Synthetic Proteins for in vivo Drug
TITLE OF INVENTION: Delivery and Tissue Augmentation
UMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
ADDRESSEE: Flehr, Hobbach, Suite 3400
                                                                                                                                                                                                                           RESULT 15
US-08-806-029-27
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                         COUNTRY: U
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Floppy disk
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618 589 530 508 453

412 397 353 341 294 285 234

471

780

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/806,029
FILING DATE: 24-FEB-1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,237
FILING DATE: 11-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31.801
REFERENCE/DOCKET NUMBER: 31.801
REFERENCE/DOCKET NUMBER: 3-58847-2/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 398-3249
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: unknown
MOLECULE TYPE: protein
US-08-806-029-27

78.0%; SCOTE 3253; DB 3;
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                                                      VGVPGVGVPGVGVPGKGVPGVG-PGVG-PGVG-PGVGPGAGAGSGAGAGSGAGAGSGAGAG
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Search completed: December 30, 2004, 12:58:12 Job time: 33 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

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15: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US10B_PUB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US10B_PUB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

13	12	11	10	9	8	7	σ	U	4.	ω	2	Ľ	Result No.
3448	3448	3448	3448	3448	3448	3448	3448	3526	4173	4173	4173	4173	Score
82.6	82.6	82.6	82.6	82.6	82.6	82.6	82.6	84.5	100.0	100.0	100.0	100.0	Query
1125	1105	1027	983	884	884	884	884	889	780	780	780	780	Query Match Length DB
17	17	17	17	17	17	16	14	8	17	17	16	15	DB BG
US-10-845-936A-34	US-10-845-936A-33	US-10-845-936A-32	US-10-845-936A-37	US-10-845-936A-25	US-10-845-775A-25	US-10-800-179-25	US-10-117-931-15	US-08-806-029-19	US-10-845-936A-19	US-10-845-775A-19	US-10-800-179-19	US-10-441-965-19	ID
•	•		Sequence 37, Appl	Sequence 25, Appl	Sequence 25, Appl	Sequence 25, Appl	Sequence 15, Appl	Sequence 19, Appl	•	•	Sequence 19, Appl	•	Description

45	44	43	42	41	40	39	38	37	36	35	34	ω u	32	31	30	29	28	27	26	25	24	23	22	21	20	. 19	18	17	16	15	
2281.5	2281.5	2420	2463	2621	2643	2654	2665.5	2676	2740	2795	2810	2814	2830	2855	2859.5	2998	3089	3158	3176	3182	3192	3250	3253	3263	3296	3305	3305	3305	3346	3346	
54.7	54.7	•	•	62.8	•	63.6	63.9	•	65.7	67.0	67.3	67.4	67.8	68.4	68.5	•		75.7	76.1	•	76.5			78.2			79.2	•		•	
1177	1136	1040	1169	1024	972	936	1011	953	966	936	696	696	750	1002	696	1056	2018	2055	1465	988	768	1043	832	1016	2257	1038	1038	1038	965	965	
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US-10-096-986-64	US-08-806-029-9	US-08-806-029-32	US-08-806-029-33	US-08-806-029-31	US-08-806-029-30	US-08-806-029-26	US-10-096-986-94	US-08-806-029-14	US-10-117-931-34	US-10-117-931-30	US-10-441-965-23	US-08-806-029-36	US-08-806-029-25	US-10-117-931-25	US-10-441-965-21	US-08-806-029-29	US-10-096-986-80	US-10-096-986-81	US-10-096-986-74	US-08-806-029-28	US-08-806-029-35	US-10-845-936A-35	US-08-806-029-27	US-10-845-936A-36	US-10-096-986-82	US-10-845-936A-30	US-10-845-775A-30	US-10-800-179-30	US-10-845-936A-31	US-10-845-775A-31	
9	Sequence 9, Appli	32	Sequence 33, Appl	31,	Sequence 30, Appl	6,	٠.	4.	Sequence 34, Appl	Sequence 30, Appl	Sequence 23, App.	w	, S	•	Sequence 21, Appl	Sequence 29, Appl	80,	Sequence 81, Appl	9 74	Sequence 28, Appl	35,	e 35	27,	36,	82	30,	Sequence 30, App.	30,	Sequence 31, App.	31,	

ALIGNMENTS

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                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: polymer US-10-441-965-19
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, Sequence 19, Application US/10441965
; Publication No. US20040014186A1
; GENERAL INFORMATION:
; APPLICANT: KUMAR, MANOJ
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Best Local Similarity
Matches 780; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: SYNTHESIS OF INORGANIC STRUCTURES USING TEMPLATION AND TITLE OF INVENTION: CATALYSIS BY SELF ASSEMBLED REPEAT PROTEIN POLYMERS FILE REFERENCE: DOC 0061 PA CURRENT APPLICATION NUMBER: US/10/441,965
CURRENT FILING DATE: 2003-05-20
PRIOR APPLICATION NUMBER: 60/381,913
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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Sequence 19, Application US/10800179

Publication No. US20040180027A1

GENERAL INFORMATION:

APPLICANT: Cuevas, William A.

APPLICANT: Kumar, Manoj

ITITLE OF INVENTION: Use of Repeat Sequence Protein Pol:

ITITLE OF INVENTION: Compositions

FILE REFERENCE: DOC 0057 PA / GC792-4 / DC 5074

CURRENT APPLICATION NUMBER: US/10/800,179

CURRENT FILING DATE: 2004-03-12

PRIOR APPLICATION NUMBER: 60/454,077

PRIOR FILING DATE: 2003-03-12

PRIOR FILING DATE: 2003-03-12

SOFTWARE: Patentin version 3.2

SEQ ID NO 19

LENGTH: 780

TYPE: PRT

ORGANISM: Unknown

FEATURE:

OTHER THEORMATION: SELD 478
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                                         ; OTHER INFORMATION: US-10-800-179-19
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US-10-845-775A-19
Sequence 19, Application US/10845775A
Publication No. US20040228913A1
GENERAL INFORMATION:
APPLICANT: Kumar, Manoj
APPLICANT: Kumar, Manoj
APPLICANT: Christiano, Steven P.
TITLE OF INVENTION: Controlled Release of Active Agents Utilizing Repeat Sequence
TITLE OF INVENTION: Protein Polymers
FILE REFERENCE: DOC 0077 PA/GC 792-6/DC 5110
CURRENT APPLICATION NUMBER: US/10/845,775A
CURRENT APPLICATION NUMBER: US/10/845,775A
CURRENT FILING DATE: 2004-05-14
PRIOR APPLICATION UNMER: US/04/05-14
PRIOR FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.2
SEQ ID NO 19
LENGTH: 780
TYPE: PRT
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RESULT 4

US-10-845-936A-19

Sequence 19, Application US/10845936A

Publication No. US20040234609A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Collier, Katherine D.

APPLICANT: Cuevas, William A.

APPLICANT: Kumar, Manoj A.

APPLICANT: Kumar, Manoj A.

TITLE OF INVENTION: Repeat Sequence Protein Polymer Active Agent Conjugates,

TITLE OF INVENTION: and Uses

FILE REFERENCE: DOC0068PA/DC5058/GC792
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Best Local Similarity 100.0%;
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Best Local S
Matches 780
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CURRENT FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: 60/470,464
PRIOR FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.2
SEQ ID NO 19
LENGTH: 780
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ORGANISM: unknown
FEATURE:
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RESULT 5 US-08-806-029-19

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TELEPAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS:
LENGTH: 889 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: unknown
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Best Local Similarity
Matches 765; Conserv
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APPLICANT: Cappello, Joseph
APPLICANT: Stedronsky, Erwin R.
APPLICANT: Stedronsky, Erwin R.
TITLE OF INVENTION: Synthetic Proteins for in vivo Drug
TITLE OF INVENTION: Delivery and Tissue Augmentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
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NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-58847-2/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE: 11-MAR-
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CORRESPONDENCE ADDRESS:
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STREET: Four Embarcadero Center, Suite 3400
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                                        United States
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11-MAR-1994
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Pred. No. 3.3e-208;
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US-10-117-931-15
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                                               TELEPHONE: 415-781-1989
TELEPAX: 415-798-3349
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                              FILING DATE: 05-Apr-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/08/642,246
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A61127-1/BI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/117,931
                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: Four Embarcadero Center, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: STEDRONSKY, Erwin R.
CAPPELLO, Joseph
TITLE OF INVENTION: Tissue Adhesive Using Synthetic
Crosslinking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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COUNTRY: US
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TYPE: amino acid
STRANDEDNESS: single
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                                 LENGTH: 884 amino acids
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RESULT 7
US-10-800-179-25
US-10-800-179-25
; Sequence 25, Application US/10800179
; Publication No. US20040180027A1
; GENERAL INFORMATION:
; APPLICANT: Cuevas, William A.
; APPLICANT: Kumar, Manoj
; TITLE OF INVENTION: Use of Repeat Se
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SEQUENCE DESCRIPTION:
US-10-117-931-15
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Pred. No. 1.9e-203;
0; Mismatches 26;
           Sequence Protein Polymers
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FILE REFERENCE: DOC 0057 PA / GC792-4 /
CURRENT APPLICATION NUMBER: US/10/800,17
CURRENT FILING DATE: 2004-03-12
PRIOR APPLICATION NUMBER: 60/454,077
PRIOR FILING DATE: 2003-03-12
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.2
SEQ ID NO 25
LENGTH: 884
TYPE: PRT
ORGANISM: Unknown
FEATURE:
ONGANISM: Unknown
SELP 47E-13
US-10-800-179-25
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                                                                                                      82.6%; Score 3448; DB 16; ilarity 90.6%; Pred. No. 1.9e-203; Conservative 0; Mismatches 26;
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; TYPE: PRT; ORGANISM: unknown; FEATURE: FEATURE: OTHER INFORMATION: artificial glycine-rich peptide repeat sequence US-10-845-775A-25
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US-10-845-775A-25
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APPLICANT: Kumar, Manoj
APPLICANT: Christiano, Steven P.
TITLE OF INVENTION: Protein Polymers
FILE REFERENCE: DOC 0077 PA/GC 79245/DC 5110
CURRENT APPLICATION NUMBER: US/10/845,775A
CURRENT FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: US 60/470,465
PRIOR APPLICATION NUMBER: US 60/470,465
PRIOR FILLING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3:2
SEQ ID NO 25
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Pred. No. 1.9e-203;
0; Mismatches 26;
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US-10-845-936A-25
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APPLICANT: Collier, Katherine D.
APPLICANT: Collier, Katherine D.
APPLICANT: Collier, Katherine D.
APPLICANT: Collier, Katherine D.
APPLICANT: Kumar, Manoj A.
APPLICANT: Kumar, Manoj A.
TITLE OF INVENTION: Repeat Sequence Protein Polymer Active Agent Conjugates, Methods
TITLE OF INVENTION: and Uses
FILE REFERENCE: DOC00688PA/DC5058/GC792
CURRENT APPLICATION NUMBER: US/10/845,936A
CURRENT APPLICATION NUMBER: US/10/845,936A
CURRENT FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: 60/470,464
PRIOR FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PATENTIN Version 3.2
SEQ ID NO 25
LENGTH: 884
TYPE: PAT
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Best Local 9
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Pred. No. 1.9e-203;
0; Mismatches 26;
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Sequence 37, Application US/10845936A

Publication No. US20040234609A1

GENERAL INFORMATION:
APPLICANT: Collier, Katherine D.
APPLICANT: Collier, Katherine D.
APPLICANT: Kumar, Manof A.

APPLICANT: Kumar, Manof A.

TITLE OF INVENTION: Repeat Sequence Protein Polymer Active Agent Conjugates, Methods
TITLE OF INVENTION: and Uses
FILE REFERENCE: DOC0068PA/DC5058/GC792
CURRENT APPLICATION NUMBER: US/10/845,936A
CURRENT FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: 60/470,464
PRIOR APPLICATION NUMBER: 60/470,464
PRIOR FILING DATE: 2003-05-14
VUMBER OF SEQ ID NOS: 37
SEQ ID NO 3: 37
LENGTH: 983
TYPE: PRT
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Matches 752; Conserv
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Pred. No. 2e-203;
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         Best Local Similarity Matches 752; Conserv
                             Query Match
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APPLICANT: COLLIER, Katherine D.
APPLICANT: Cuevas, William A.
APPLICANT: Cuevas, William A.
APPLICANT: Cuevas, William A.
APPLICANT: Kumar, Manoj A.
TITLE OF INVENTION: Repeat Sequence Protein Pol
TITLE OF INVENTION: and Uses
FILE REFERENCE: DOCO068PAD.C55058/GC792
CURRENT APPLICATION NUMBER: US/10/845,936A
CURRENT FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: 60/470,464
PRIOR FILING DATE: 2003-05-14
PRIOR FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 37
SOPTWARE: Patentin version 3.2
SEQ ID NO 32
SEQ ID NO 32
LENGTH: 1027
TYPE: PRT
ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION:
US-10-845-936A-32
                                                                                                                                                                                                                                                                                                                                 US-10-845-936A-32
                                                                                                                                                                                                                                                                                   Sequence 32, Application US/10845936A Publication No. US20040234609A1 GENERAL INFORMATION:
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Conservative

90.6%;

Score 3448; DB 17; Pred. No. 2.1e-203; 0; Mismatches 26;

Length 1027;

Indels

52;

Gaps

52;

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Sequence 33, Application US/10845936A

Publication No. US20040234609A1

GENERAL INFORMATION:

APPLICANT: COLLIER, Katherine D.

APPLICANT: Cuevas, William A.

APPLICANT: Kumar, Manoj A.

ITITLE OF INVENTION: Repeat Sequence Protein Pol

ITITLE OF INVENTION: and Uses

ITITLE OF INVENTION: AND USES GCC792

CURRENT APPLICATION NUMBER: US/10/845,936A

CURRENT FILING DATE: 2004-05-14

PRIOR APPLICATION NUMBER: 60/470,464

PRIOR PILING DATE: 2003-05-14

PRIOR PILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 37
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; SEQ ID NO 33
; LENGTH: 1105
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
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Best Local Similarity
Matches 752; Conser
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Pred. No. 2.2e-203;
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GENERAL INFORMATION:
APPLICANT: Collier, Katherine D.
APPLICANT: Cuevas, William A.
APPLICANT: Kumar, Manoj A.
TITLE OF INVENTION: Repeat Sequence Protein Polymer Active Agent Conjugates, Meth
TITLE OF INVENTION: and Uses
FILE REFERENCE: DOC0068PA/DC5058/GC792
CURRENT APPLICATION NUMBER: US/10/845,936A
CURRENT FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: 60/470,464
PRIOR APPLICATION ONUMBER: 05-14
PRIOR APPLICATION ONUMBER: 05-14
SOFTWARE: Patentin version 3.2
SEQ ID NO 34
LENGTH: 1125
TYPE: PRI

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Best Local Similarity 90.0
Matches 752; Conservative
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Pred. No. 2.3e-203;
0; Mismatches 26;
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RESULT 14
US-10-800-179-31
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SOFTWARE: Patentin version 3.2
SEQ ID NO 31
LENGTH: 965
TYPE: PRT
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Best Local Similarity 82.9%;
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APPLICANT: Kumar, Manoj
TITLE OF INVENTION: Use of Repeat Sequence Protein
TITLE OF INVENTION: Compositions
FILE REFERENCE: DOC 0057 PA / GC792-4 / DC 5074
CURRENT APPLICATION NUMBER: US/10/800,179
CURRENT APPLICATION NUMBER: 50/454,077
PRIOR APPLICATION NUMBER: 60/454,077
PRIOR FILING DATE: 2003-03-12
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APPLICANT: Kumar, Manoj
APPLICANT: Marceud, Isabelle
APPLICANT: Christiano, Steven P.
APPLICANT: Christiano, Steven P.
APPLICANT: Christiano, Steven P.
TITLE OF INVENTION: Controlled Release of Active Agents Utilizing Repeat Sequence of Invention: Protein Polymers
FILE REFERENCE: DOC 0077 PA/GC 792-6/DC 5110
CURRENT APPLICATION NUMBER: US/01/845,775A
CURRENT FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: US 60/470,465
PRIOR FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 31
SOPTWARE: PatentIn version 3.2
SEQ ID NO 31
LENGTH: 965
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Matches 74
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ORGANISM: unknown
FEATURE:
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Search completed: December 30, 2004, 13:01:33 Job time : 154 secs